

6FFLSPEAKLQPeayes-902-seq1.rag

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OM protein - protein search, using sw model

Run on: January 29, 2003, 12:57:01 ; Search time 35 Seconds  
(without alignments)  
53.300 Million cell updates/sec

Title: MAYES-902-SEQ1  
Perfect score: 70  
Sequence: 1 gseflepeaklqpr 14

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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22: /SID52/gcgdata/geneseq/emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 66    | 94.3        | 14     | AAU76321  | Synthetic Ghrelin  |
| 2          | 53.5  | 76.4        | 27     | AAAB60514 | Rat des-Gln14-ghre |
| 3          | 53.5  | 76.4        | 27     | AAAB60515 | Human des-Gln14-gh |
| 4          | 53.5  | 76.4        | 116    | AAAB60516 | Rat des-Gln14-ghre |
| 5          | 53.5  | 76.4        | 116    | AAAB60517 | Human des-Gln14-gh |
| 6          | 53    | 75.7        | 28     | AAAG4993  | Neurone denaturati |
| 7          | 53    | 75.7        | 28     | AAAB60508 | Rat ghrelin, SEQ I |
| 8          | 53    | 75.7        | 28     | AAAB60509 | Human ghrelin, SEQ |
| 9          | 53    | 75.7        | 28     | AAAB60530 | Dog ghrelin-like G |
| 10         | 53    | 75.7        | 28     | AAE19032  | Human ghrelin pept |

|    |      |      |     |    |           |                     |
|----|------|------|-----|----|-----------|---------------------|
| 11 | 53   | 75.7 | 28  | 23 | AAE19041  | Human ghrelin pept  |
| 12 | 53   | 75.7 | 90  | 23 | ABP08975  | Human ORFX protein  |
| 13 | 53   | 75.7 | 117 | 20 | AAW87991  | Protein designated  |
| 14 | 53   | 75.7 | 117 | 21 | AAW87236  | Human signal pept   |
| 15 | 53   | 75.7 | 117 | 22 | AAW38890  | Human polypeptide   |
| 16 | 53   | 75.7 | 117 | 22 | AAAB62649 | Human zsig33 polyp  |
| 17 | 53   | 75.7 | 117 | 22 | AAAB20101 | Zsig33 protein, H   |
| 18 | 53   | 75.7 | 117 | 22 | AAAB60510 | Rat ghrelin prepro  |
| 19 | 53   | 75.7 | 117 | 22 | AAAB60511 | Human ghrelin prep  |
| 20 | 53   | 75.7 | 117 | 23 | AAE23838  | Human zsig33 prote  |
| 21 | 53   | 75.7 | 117 | 23 | AAE15883  | Human zsig33 prote  |
| 22 | 53   | 75.7 | 118 | 21 | AAI66708  | Membrane-bound pro  |
| 23 | 53   | 75.7 | 118 | 22 | AAV12392  | Human PRO1066 poly  |
| 24 | 53   | 75.7 | 118 | 22 | AAAB65231 | Human polypeptide   |
| 25 | 53   | 75.7 | 126 | 22 | AAW40676  | Porcine des-Gln14-  |
| 26 | 49.5 | 70.7 | 27  | 22 | AAAB60519 | Porcine des-Gln14-  |
| 27 | 49.5 | 70.7 | 117 | 22 | AAAB60521 | Porcine ghrelin, S  |
| 28 | 49   | 70.0 | 28  | 22 | AAAB60518 | Rat ghrelin-deriva  |
| 29 | 49   | 70.0 | 28  | 22 | AAAB60560 | Human ghrelin pept  |
| 30 | 49   | 70.0 | 28  | 23 | AAE19021  | Human ghrelin pept  |
| 31 | 49   | 70.0 | 28  | 23 | AAE19027  | Human ghrelin pept  |
| 32 | 49   | 70.0 | 28  | 23 | AAE19028  | Human ghrelin pept  |
| 33 | 49   | 70.0 | 28  | 23 | AAE19029  | Human ghrelin pept  |
| 34 | 49   | 70.0 | 28  | 23 | AAE19030  | Human ghrelin pept  |
| 35 | 49   | 70.0 | 28  | 23 | AAE19031  | Human ghrelin pept  |
| 36 | 49   | 70.0 | 28  | 23 | AAE19033  | Human ghrelin pept  |
| 37 | 49   | 70.0 | 28  | 23 | AAE19034  | Human ghrelin pept  |
| 38 | 49   | 70.0 | 28  | 23 | AAE19035  | Human ghrelin pept  |
| 39 | 49   | 70.0 | 28  | 23 | AAE19036  | Human ghrelin pept  |
| 40 | 49   | 70.0 | 28  | 23 | AAE19037  | Human ghrelin pept  |
| 41 | 49   | 70.0 | 28  | 23 | AAE19038  | Human ghrelin pept  |
| 42 | 49   | 70.0 | 28  | 23 | AAE19039  | Human ghrelin pept  |
| 43 | 49   | 70.0 | 28  | 23 | AAE19040  | Human ghrelin pept  |
| 44 | 49   | 70.0 | 118 | 22 | AAAB60520 | Porcine ghrelin, pr |
| 45 | 44   | 62.9 | 23  | 22 | AAAB60528 | Rainbow trout 23aa  |

ALIGNMENTS

|          |  |
|----------|--|
| RESULT 1 |  |
| AAU76321 | AAU76321 standard; peptide; 14 AA.                                   |
| ID       | AAU76321;  |
| AC       | AAU76321;  |
| XX       |  |
| DT       | 21-MAY-2002 (first entry)  |
| XX       |  |
| DE       | Synthetic Ghrelin variant #3.  |
| XX       |  |
| KW       | Ghrelin; antagonist; growth hormone release; octanoyl ester; tumour; |
| KW       | acromegaly; osteopetrotic.   |
| XX       |  |
| OS       | Synthetic.   |
| XX       |  |
| FH       | Key  |
| FT       | Modified-site 3  |
| FT       | /label= OTHER  |
| FT       | /note= "Other= Octanoyl Ser"   |
| XX       |  |
| PN       | WO200208250-A2.  |
| PD       | 31-JAN-2002.   |
| XX       |  |
| PF       | 10-JUL-2001; 2001WO-EP07929.   |
| XX       |  |
| PR       | 24-JUL-2000; 2000US-220178P.   |
| XX       |  |
| PA       | (ZENT-) ZENTARIS AG.   |
| PI       | Deghenght R;   |
| XX       |  |
| XX       | WPI; 2002-206079/26.   |

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XX New peptide which antagonises the effect of ghrelin when administered
PT to a mammal
XX
XX Claim 3; Page 6; 9pp; English.
PS
CC The invention relates to a novel peptide which antagonises the effect of
CC ghrelin when administered to a mammal. The peptide is a synthetic
CC analogue of ghrelin. Ghrelin is a 27-28 residue peptide isolated
CC from distinctive cell types in the stomach of rats and humans and has an
CC octanoyl ester attached to a serine residue. Ghrelin is a potent
CC releaser of growth hormone. The peptides are useful for normalising
CC elevated growth hormone levels in mammals such as those suffering
CC from a tumour related to overproduction of growth hormone or acromegaly.
CC The present sequence is a ghrelin antagonising peptide of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match 94.3%; Score 66; DB 23; Length 14;
Best Local Similarity 92.9%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSSFLSPPEAKLQPR 14
Db 1 GSKFLSPPEAKLQPR 14

RESULT 2
AAB60514
ID AAB60514 standard; peptide; 27 AA.
XX
XX AAB60514;
XX
DT 24-APR-2001 (first entry)
XX
DE Rat des-Gln14-ghrelin, SEQ ID NO:10.
XX
XX Growth hormone secretagogue; GHS; ghrelin;
XX calcium concentration elevation; infant growth disorder;
XX growth hormone deficiency.
XX
XX Rattus norvegicus.
XX
XX WO200107475-A1.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000WO-JP04907.
XX
XX 23-JUL-1999; 99JP-0210002.
XX
XX 29-NOV-1999; 99JP-0338841.
XX
XX 26-APR-2000; 2000JP-0126623.
XX
XX (KANG/) KANGAWA K.
XX
XX Kangawa K, Kojima M, Hosoda H, Matsu H, Minamitake Y;
XX
XX WPI; 2001-159704/16.
XX
XX New peptide compounds which induce growth hormone secretion and
XX elevate cell calcium concentrations, useful in treatment and diagnosis
XX of infant growth disorders -
XX
XX Claim 3; Page 185; 210pp; Japanese.
XX
XX The invention relates to a novel peptide compound or its salt which
XX induces the secretion of growth hormone and/or elevates calcium ion
XX concentration in cells. The peptides are ghrelin homologues and are
XX characterised in that at least one amino acid has been substituted by
XX a modified amino acid and/or a non-amino acid compound. The invention
XX also encompasses the unmodified peptides; the DNA encoding the peptides;
XX vectors and host cells comprising such DNA; a method of producing the
XX

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CC peptides comprising recombinant production, optionally followed by
CC chemical modification; an antibody specific for a peptide of the
CC invention; and an assay and kit for detecting the peptides. The peptides
CC of the invention are useful for treating and/or diagnosing diseases
CC caused by a deficiency in growth hormone expression or activity. In
CC particular, they are useful for promoting infant growth due to growth
CC hormone deficiency. The compounds of the invention are safe with
CC ghrelin-type growth hormone secretagogue (GHS) of the invention.
XX
SQ Sequence 27 AA;

Query Match 76.4%; Score 53.5; DB 22; Length 27;
Best Local Similarity 51.9%; Pred. No. 0.035;
Matches 14; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 GSSFLSPPE-----AKLQPR 14
Db 1 GSSFLSPPEHOKAKRKESKKPKLQPR 27

RESULT 3
AAB60515
ID AAB60515 standard; peptide; 27 AA.
XX
XX AAB60515;
XX
XX 24-APR-2001 (first entry)
XX
XX Human des-Gln14-ghrelin, SEQ ID NO:11.
XX
XX Growth hormone secretagogue; GHS; ghrelin;
XX calcium concentration elevation; infant growth disorder;
XX growth hormone deficiency.
XX
XX Homo sapiens.
XX
XX WO200107475-A1.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000WO-JP04907.
XX
XX 23-JUL-1999; 99JP-0210002.
XX
XX 29-NOV-1999; 99JP-0338841.
XX
XX 26-APR-2000; 2000JP-0126623.
XX
XX (KANG/) KANGAWA K.
XX
XX Kangawa K, Kojima M, Hosoda H, Matsu H, Minamitake Y;
XX
XX WPI; 2001-159704/16.
XX
XX New peptide compounds which induce growth hormone secretion and
XX elevate cell calcium concentrations, useful in treatment and diagnosis
XX of infant growth disorders -
XX
XX Claim 3; Page 185; 210pp; Japanese.
XX
XX The invention relates to a novel peptide compound or its salt which
XX induces the secretion of growth hormone and/or elevates calcium ion
XX concentration in cells. The peptides are ghrelin homologues and are
XX characterised in that at least one amino acid has been substituted by
XX a modified amino acid and/or a non-amino acid compound. The invention
XX also encompasses the unmodified peptides; the DNA encoding the peptides;
XX peptides comprising recombinant production, optionally followed by
XX chemical modification; an antibody specific for a peptide of the
XX invention; and an assay and kit for detecting the peptides. The peptides
XX of the invention are useful for treating and/or diagnosing diseases
XX caused by a deficiency in growth hormone expression or activity. In
XX particular, they are useful for promoting infant growth due to growth
XX hormone deficiency. The compounds of the invention are safe with
XX

```

CC no accompanying side effects. The present sequence represents a  
CC ghrelin-type growth hormone secretagogue (GHS) of the invention.  
XX  
SQ Sequence 27 AA;

Query Match 76.4%; Score 53.5; DB 22; Length 27;  
Best Local Similarity 51.9%; Pred. No. 0.035;  
Matches 14; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

OY 1 GSSFLSPK-----AKLQPR 14  
|||  
Db 1 GSSFLSPHQVQKSKKPPAKLQPR 27

RESULT 4  
AAB60516  
ID AAB60516 standard; Protein; 116 AA.

AC AAB60516;

DT 24-APR-2001 (first entry)

XX Rat des-Gln14-ghrelin preproprotein, SEQ ID NO:12.

XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;

KM calcium concentration elevation; infant growth disorder;

XX growth hormone deficiency.

OS Rattus norvegicus.

XX WO200107475-A1.

PD 01-FEB-2001.

XX 24-JUL-2000; 2000MO-JP04907.

PR 23-JUL-1999; 99JP-0210002.

PR 29-NOV-1999; 99JP-0338841.

PR 26-APR-2000; 2000JP-0126623.

XX (KANG/) KANGAWA K.

PI Kangawa K, Kojima M, Hosoda H, Matsu H, Minamitake Y;

DR WPI; 2001-159704/16.

XX N-PSDB; AAF59646.

PS Claim 3; Page 186; 210pp; Japanese.

XX The invention relates to a novel peptide compound or its salt which

CC induces the secretion of growth hormone and/or elevates calcium ion

CC concentration in cells. The peptides are ghrelin homologues and are

CC characterised in that at least one amino acid has been substituted by

CC a modified amino acid and/or a non-amino acid compound. The invention

CC also encompasses the unmodified peptides; the DNA encoding the peptides;

CC vectors and host cells comprising such DNA; a method of producing the

CC peptides comprising recombinant production, optionally followed by

CC chemical modification; an antibody specific for a peptide of the

CC invention; and an assay and kit for detecting the peptides. The peptides

CC caused by a deficiency in growth hormone expression or activity. In

CC particular, they are useful for promoting infant growth due to growth

CC hormone deficiency. The compounds of the invention are safe with

CC no accompanying side effects. The present sequence represents a

CC ghrelin-type growth hormone secretagogue (GHS) precursor protein

CC of the invention.

XX Sequence 116 AA;

SQ

Query Match 76.4%; Score 53.5; DB 22; Length 116;  
Best Local Similarity 51.9%; Pred. No. 0.17;  
Matches 14; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

OY 1 GSSFLSPK-----AKLQPR 14  
|||  
Db 24 GSSFLSPHQVQKSKKPPAKLQPR 50

RESULT 5  
AAB60517  
ID AAB60517 standard; Protein; 116 AA.

AC AAB60517;

DT 24-APR-2001 (first entry)

XX Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.

XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;

KM calcium concentration elevation; infant growth disorder;

XX growth hormone deficiency.

OS Homo sapiens.

XX WO200107475-A1.

PD 01-FEB-2001.

XX 24-JUL-2000; 2000MO-JP04907.

PR 23-JUL-1999; 99JP-0210002.

PR 29-NOV-1999; 99JP-0338841.

PR 26-APR-2000; 2000JP-0126623.

XX (KANG/) KANGAWA K.

PI Kangawa K, Kojima M, Hosoda H, Matsu H, Minamitake Y;

DR WPI; 2001-159704/16.

XX N-PSDB; AAF59647.

PS Claim 3; Page 186-187; 210pp; Japanese.

XX The invention relates to a novel peptide compound or its salt which

CC induces the secretion of growth hormone and/or elevates calcium ion

CC concentration in cells. The peptides are ghrelin homologues and are

CC characterised in that at least one amino acid has been substituted by

CC a modified amino acid and/or a non-amino acid compound. The invention

CC also encompasses the unmodified peptides; the DNA encoding the peptides;

CC vectors and host cells comprising such DNA; a method of producing the

CC peptides comprising recombinant production, optionally followed by

CC chemical modification; an antibody specific for a peptide of the

CC invention; and an assay and kit for detecting the peptides. The peptides

CC caused by a deficiency in growth hormone expression or activity. In

CC particular, they are useful for promoting infant growth due to growth

CC hormone deficiency. The compounds of the invention are safe with

CC no accompanying side effects. The present sequence represents a

CC ghrelin-type growth hormone secretagogue (GHS) precursor protein

CC of the invention.

XX Sequence 116 AA;

SQ

Query Match 76.4%; Score 53.5; DB 22; Length 116;  
Best Local Similarity 51.9%; Pred. No. 0.17;  
Matches 14; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

OY 1 GSSFLSPK-----AKLQPR 14

Db 24 GSSFLSPFHQVQRKESKKPKAKLQPR 50

## RESULT 6

AA664943 ID AAG64943 standard; peptide; 28 AA.

AC AAG64943;

DT 19-OCT-2001 (first entry)

DE Neurone denaturation prevention method related peptide #5.

KM Neurone denaturation; neurone death; growth hormone liberation inhibitor;

KM cerebral infarction; oedema; Alzheimer's disease; Parkinson's disease;

KM Pick's disease; dementia; amyotrophic lateral sclerosis; cancer;

KM diabetic neuropathy; neuroprotective; antiinflammatory; nootropic;

OS cyostatic.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 3 /label= OTHER

FT /note= "modified by O(C=O) (CH2) 6CH3"

PN WO200147558-A1.

XX 05-JUL-2001.

PE 28-DEC-2000; 2000WO-JP09431.

PR 28-DEC-1999; 99JP-0375513.

PA (KAKE) KAKEN PHARM CO LTD.

PI Murata T, Ohyama T, Amakawa M, Fujita K, Ueo H;

DR WPI; 2001-536280/59.

PT Agents for treating diseases associated with denaturation or death of

XX neurons comprise growth hormone liberation inhibitor

PS Disclosure; Page 17; 50pp; Japanese.

CC The present invention provides agents for treating or preventing diseases

CC associated with denaturation or death of neurons, which comprise a

CC growth hormone liberation inhibitor. These can be used for treating or

CC preventing diseases associated with denaturation or death of neurons

CC including those due to cerebral ischaemic disorders such as cerebral

CC infarction or oedema. Other causes of denaturation or death of neurons

CC included Alzheimer's disease, Pick's disease, AIDS related dementia,

CC Parkinson's disease, amyotrophic lateral sclerosis, diabetic neuropathy

CC and anticancer treatments. The present sequence is a peptide described in

CC the exemplification of the invention.

XX Sequence 28 AA;

QY 1 GSSFLSPF-----AKLQPR 14

Db 1 GSSFLSPFHQVQRKESKKPKAKLQPR 28

## RESULT 7

AA660508

ID AAB60508 standard; peptide; 28 AA.

XX AAB60508;

AC AAB60508;

XX 24-APR-2001 (first entry)

DT Rat ghrelin, SEQ ID NO:2.

XX Growth hormone secretagogue; GHS; ghrelin;

KM calcium concentration elevation; infant growth disorder;

XX growth hormone deficiency.

OS Rattus norvegicus.

XX WO200107475-A1.

PN 01-FEB-2001.

PD 24-JUL-2000; 2000WO-JP04907.

PR 23-JUL-1999; 99JP-0210002.

PR 29-NOV-1999; 99JP-0338841.

PR 26-APR-2000; 2000JP-0126623.

XX (KANG/) KANGAWA K.

PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;

XX WPI; 2001-159704/16.

PT New peptide compounds which induce growth hormone secretion and

PT elevate cell calcium concentrations, useful in treatment and diagnosis

XX of infant growth disorders

PS Claim 2; Page 180; 210pp; Japanese.

XX The invention relates to a novel peptide compound or its salt which

CC induces the secretion of growth hormone and/or elevates calcium ion

CC concentration in cells. The peptides are ghrelin homologues and are

CC characterised in that at least one amino acid has been substituted by

CC a modified amino acid and/or a non-amino acid compound. The invention

CC also encompasses the unmodified peptides; the DNA encoding the peptides;

CC vectors and host cells comprising such DNA; a method of producing the

CC peptides comprising recombinant production, optionally followed by

CC chemical modification; an antibody specific for a peptide of the

CC invention; and an assay and kit for detecting the peptides. The peptides

CC of the invention are useful for treating and/or diagnosing diseases

CC caused by a deficiency in growth hormone expression or activity. In

CC particular, they are useful for promoting infant growth due to growth

CC hormone deficiency. The compounds of the invention are safe with

CC no accompanying side effects. The present sequence represents a

XX ghrelin-type growth hormone secretagogue (GHS) of the invention.

XX Sequence 28 AA;

QY 1 GSSFLSPF-----AKLQPR 14

Db 1 GSSFLSPFHQVQRKESKKPKAKLQPR 28

QY 1 GSSFLSPF-----AKLQPR 14

Db 1 GSSFLSPFHQVQRKESKKPKAKLQPR 28

QY 1 GSSFLSPF-----AKLQPR 14

Db 1 GSSFLSPFHQVQRKESKKPKAKLQPR 28

AC AAB60509;

DT 24-APR-2001 (first entry)

XX Human ghrelin, SEQ ID NO:3.

KM Growth hormone secretagogue; GHS; ghrelin;

KM calcium concentration elevation; infant growth disorder;

KM growth hormone deficiency.  
 XX  
 PF Homo sapiens.  
 OS  
 XX WO200107475-A1.  
 PN  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 24-JUL-2000; 2000WO-JP04907.  
 XX  
 PR 23-JUL-1999; 99JP-0210002.  
 PR 29-NOV-1999; 99JP-0338841.  
 PR 26-APR-2000; 2000JP-0126623.  
 XX  
 PA (KANG/) KANGAWA K.  
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;  
 DR WPI; 2001-159704/16.  
 XX  
 PT New peptide compounds which induce growth hormone secretion and  
 PT elevate cell calcium concentrations, useful in treatment and diagnosis  
 of infant growth disorders -  
 PS Claim 3; Page 181; 210pp; Japanese.  
 XX  
 CC The invention relates to a novel peptide compound or its salt which  
 CC induces the secretion of growth hormone and/or elevates calcium ion  
 CC concentration in cells. The peptides are ghrelin homologues and are  
 CC characterised in that at least one amino acid has been substituted by  
 CC a modified amino acid and/or a non-amino acid compound. The invention  
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;  
 CC vectors and host cells comprising such DNA; a method of producing the  
 CC peptides comprising recombinant production, optionally followed by  
 CC chemical modification; an antibody specific for a peptide of the  
 CC invention; and an assay and kit for detecting the peptides. The peptides  
 CC of the invention are useful for treating and/or diagnosing diseases  
 CC caused by a deficiency in growth hormone expression or activity. In  
 CC particular, they are useful for promoting infant growth due to growth  
 CC hormone deficiency. The compounds of the invention are safe with  
 CC no accompanying side effects. The present sequence represents a  
 CC ghrelin-type growth hormone secretagogue (GHS) of the invention.  
 XX  
 SQ Sequence 28 AA;  
 XX  
 Query Match 75.7%; Score 53; DB 22; Length 28;  
 Best Local Similarity 50.0%; Pred. NO. 0.044;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 QY 1 GSSFLSP-----AKLQPR 14  
 DB 1 GSSFLSPHQKQQRKSKKPKAKLQPR 28  
 XX  
 RESULT 9  
 AAB60530  
 ID AAB60530 standard; peptide; 28 AA.  
 XX  
 AC AAB60530;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Dog ghrelin-like GH secretagogue peptide, SEQ ID NO:31.  
 XX  
 KM Growth hormone secretagogue; GHS; ghrelin.  
 KM calcium concentration elevation; infant growth disorder;  
 KM growth hormone deficiency.  
 XX  
 OS Canis familiaris.  
 OS  
 PN WO200107475-A1.  
 XX  
 PD 01-FEB-2001.  
 XX

XX  
 XX 24-JUL-2000; 2000WO-JP04907.  
 XX  
 PR 23-JUL-1999; 99JP-0210002.  
 PR 29-NOV-1999; 99JP-0338841.  
 PR 26-APR-2000; 2000JP-0126623.  
 XX  
 PA (KANG/) KANGAWA K.  
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;  
 DR WPI; 2001-159704/16.  
 XX  
 PT New peptide compounds which induce growth hormone secretion and  
 PT elevate cell calcium concentrations, useful in treatment and diagnosis  
 of infant growth disorders -  
 PS Claim 4; Page 197; 210pp; Japanese.  
 XX  
 CC The invention relates to a novel peptide compound or its salt which  
 CC induces the secretion of growth hormone and/or elevates calcium ion  
 CC concentration in cells. The peptides are ghrelin homologues and are  
 CC characterised in that at least one amino acid has been substituted by  
 CC a modified amino acid and/or a non-amino acid compound. The invention  
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;  
 CC vectors and host cells comprising such DNA; a method of producing the  
 CC peptides comprising recombinant production, optionally followed by  
 CC chemical modification; an antibody specific for a peptide of the  
 CC invention; and an assay and kit for detecting the peptides. The peptides  
 CC of the invention are useful for treating and/or diagnosing diseases  
 CC caused by a deficiency in growth hormone expression or activity. In  
 CC particular, they are useful for promoting infant growth due to growth  
 CC hormone deficiency. The compounds of the invention are safe with  
 CC no accompanying side effects. The present sequence represents a  
 CC ghrelin-type growth hormone secretagogue (GHS) of the invention.  
 XX  
 SQ Sequence 28 AA;  
 XX  
 Query Match 75.7%; Score 53; DB 22; Length 28;  
 Best Local Similarity 50.0%; Pred. NO. 0.044;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 QY 1 GSSFLSP-----AKLQPR 14  
 DB 1 GSSFLSPHQKQQRKSKKPKAKLQPR 28  
 XX  
 RESULT 10  
 AAE19032  
 ID AAE19032 standard; peptide; 28 AA.  
 XX  
 AC AAE19032;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX  
 DE Human ghrelin peptide analogue, compound 6.  
 XX  
 KM Human; ghrelin analogue; growth-hormone secretagogue; GHS receptor; AIDS;  
 KM acquired immune deficiency syndrome; weight gain; chemotherapy; dialysis;  
 KM growth hormone; muscle mass; bone density; sexual dysfunction; anorexia;  
 KM wasting; radiation therapy; diabetes; retinopathy; hypertension;  
 KM cardiovascular disorder; gall stone; osteoarthritis; cancer; cycostatic;  
 KM metabolic; immunomodulator; anti-HIV; anorectic; ophthalmological;  
 KM cardiant; litholytic; hepatotropic.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200192292-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US17026.  
 XX

```

PR 30-MAY-2000; 2000US-207920P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Bednarek M;
XX
XX WPI; 2002-195531/25.
XX
XX Truncated ghrelin analogs active at growth-hormone secretagogue
XX PT receptor useful for diagnosing or treating diseases such as anorexia,
XX PT bulimia, cancer, obesity, diabetes mellitus, hypertension,
XX PT osteoarthritis -
XX
XX Example 4; Page 34; 37pp; English.
XX
XX The present invention relates to a truncated ghrelin analogue or their
XX salt, active at growth-hormone secretagogue (GHS) receptor. Ghrelin
XX analogue is useful for screening a compound capable of binding to GHS
XX receptor and for stimulating growth hormone secretion. Ghrelin agonist
XX is utilised for treating a growth hormone deficient state, increasing
XX muscle mass and bone density, treating sexual dysfunction in males or
XX females, facilitating a weight gain, maintenance of weight, maintenance
XX of physical functioning, recovery of physical function, and/or appetite
XX increase, or appetite increase is particularly useful for a patient
XX having a disease or disorder, or under going a treatment, accompanied by
XX eight loss such as anorexia, bulimia, cancer cachexia, acquired
XX immune deficiency syndrome (AIDS), wasting, cachexia and wasting in frail
XX elderly and examples of treatments accompanied by weight loss include
XX chemotherapy, radiation therapy, temporary or permanent immobilisation
XX and dialysis, and ghrelin antagonist is utilised to facilitate weight
XX loss, appetite decrease, weight maintenance, treat obesity, diabetes and
XX complications of diabetes including retinopathy, and/or cardiovascular
XX disorders, where excessive weight is a contributing factor to different
XX diseases including hypertension, diabetes, dyslipidemias, cardiovascular
XX disease, gall stones, osteoarthritis and certain forms of cancers, and
XX bringing about a weight loss can be used for e.g. to reduce the
XX likelihood of such diseases and for treating such diseases. Ghrelin
XX analogue induces growth hormone release from primary-culture pituitary
XX cells in a dose-dependent manner without stimulating the release of other
XX pituitary hormones. Unlike longer length ghrelin, ghrelin analogue can be
XX synthesised easily and has increased solubility in physiological buffers.
XX The present sequence is human ghrelin peptide analogue.
XX
XX Sequence 28 AA;
XX
XX Query Match 75.7%; Score 53; DB 23; Length 28;
XX Best Local Similarity 50.0%; Pred. NO. 0.044;
XX Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
XX
XX 1 GSSFLSPF-----AKQPR 14
XX |||||
XX 1 GSSFLSPHQVRVQQRKXKPPAKQPR 28
XX
XX RESULT 11
XX ID AAE19041 standard; peptide: 28 AA.
XX AC AAE19041;
XX XX
XX DT 21-MAY-2002 (first entry)
XX
XX DE Human ghrelin peptide analogue, compound 17.
XX
XX XX Human; ghrelin analogue; growth-hormone secretagogue; GHS receptor; AIDS;
XX XX acquired immune deficiency syndrome; weight gain; chemotherapy; dialysis;
XX XX growth hormone; muscle mass; bone density; sexual dysfunction; anorexia;
XX XX wasting; radiation therapy; obesity; diabetes; retinopathy; hypertension;
XX XX cardiovascular disorder; gall stone; osteoarthritis; cancer; cytostatic;
XX XX metabolic; immunomodulator; anti-HIV; anorectic; ophthalmological;
XX XX cardiac; litholytic; hepatotropic.
XX
XX OS Homo sapiens.

```

```

XX
XX Key Location/Qualifiers
XX FT Modified-site 3
XX FT /note= "Ser(CO-(CH2)6-CH3)"
XX
XX WO200192292-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US17026.
XX
XX 30-MAY-2000; 2000US-207920P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Bednarek M;
XX
XX WPI; 2002-195531/25.
XX
XX Truncated ghrelin analogs active at growth-hormone secretagogue
XX PT receptor useful for diagnosing or treating diseases such as anorexia,
XX PT bulimia, cancer, obesity, diabetes mellitus, hypertension,
XX PT osteoarthritis -
XX
XX Example 4; Page 23; 37pp; English.
XX
XX The present invention relates to a truncated ghrelin analogue or their
XX salt, active at growth-hormone secretagogue (GHS) receptor. Ghrelin
XX analogue is useful for screening a compound capable of binding to GHS
XX receptor and for stimulating growth hormone secretion. Ghrelin agonist
XX is utilised for treating a growth hormone deficient state, increasing
XX muscle mass and bone density, treating sexual dysfunction in males or
XX females, facilitating a weight gain, maintenance of weight, maintenance
XX of physical functioning, recovery of physical function, and/or appetite
XX increase, or appetite increase is particularly useful for a patient
XX having a disease or disorder, or under going a treatment, accompanied by
XX eight loss such as anorexia, bulimia, cancer cachexia, acquired
XX immune deficiency syndrome (AIDS), wasting, cachexia and wasting in frail
XX elderly and examples of treatments accompanied by weight loss include
XX chemotherapy, radiation therapy, temporary or permanent immobilisation
XX and dialysis, and ghrelin antagonist is utilised to facilitate weight
XX loss, appetite decrease, weight maintenance, treat obesity, diabetes and
XX complications of diabetes including retinopathy, and/or cardiovascular
XX disorders, where excessive weight is a contributing factor to different
XX diseases including hypertension, diabetes, dyslipidemias, cardiovascular
XX disease, gall stones, osteoarthritis and certain forms of cancers, and
XX bringing about a weight loss can be used for e.g. to reduce the
XX likelihood of such diseases and for treating such diseases. Ghrelin
XX analogue induces growth hormone release from primary-culture pituitary
XX cells in a dose-dependent manner without stimulating the release of other
XX pituitary hormones. Unlike longer length ghrelin, ghrelin analogue can be
XX synthesised easily and has increased solubility in physiological buffers.
XX The present sequence is human ghrelin peptide analogue.
XX
XX Sequence 28 AA;
XX
XX Query Match 75.7%; Score 53; DB 23; Length 28;
XX Best Local Similarity 50.0%; Pred. NO. 0.044;
XX Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
XX
XX 1 GSSFLSPF-----AKQPR 14
XX |||||
XX 1 GSSFLSPHQVRVQQRKXKPPAKQPR 28
XX
XX RESULT 12
XX ID ABP08975 standard; Protein; 90 AA.
XX AC ABP08975;
XX XX
XX DT 24-JUN-2002 (first entry)
XX

```

DE Human ORFX protein sequence SEQ ID NO:17932.  
XX  
XX Human, open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
KM hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
KM degenerative disorder; osteoarthritis; neurodegenerative disorder;  
KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
KM hypertension; hypothyroidism; cholesterol ester storage disease;  
KM immune deficiency; immune disorder; infectious disease;  
KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
KM myasthenia gravis.  
XX  
XX Homo sapiens.  
OS  
PN WO200192523-A2.  
XX  
XX 06-DEC-2001.  
PD  
XX  
XX 29-MAY-2001; 2001MO-US10836.  
PF  
XX  
XX 30-MAY-2000; 2000US-206132P.  
PR  
XX 29-AUG-2000; 2000US-228716P.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shinkets RA, Leach MD;  
PI  
XX WPI; 2002-106308/14.  
DR N-PSDB; ABN24727.  
XX  
XX Novel human polypeptides and polynucleotides useful for diagnosing,  
PT preventing and treating cardiovascular disease, neurodegenerative,  
PT hyperproliferative disorders and autoimmune disorders -  
XX  
XX Disclosure; SEQ ID 17932; 1037pp; English.  
XX  
XX The present invention describes substantially purified human proteins  
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
CC in the specification)). ABN15762 to ABN27252 encode the human ORFX  
CC protein given in ABP00010 to ABP15500. ORFX proteins are useful for  
CC treating or preventing a pathology associated with an ORFX-associated  
CC disorder in humans, and in the manufacture of a medicament for treating a  
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
CC sequences can be used in gene therapy. ORFX sequences can be used in the  
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,  
CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
CC storage disease, various immune deficiencies and disorders, infectious  
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
CC bone degenerative disorders, or periodontal disease, and for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues and conditions resulting from  
CC systemic cytokine damage.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIFO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX  
SQ Sequence 90 AA;  
Query Match 75.7%; Score 53; DB 23; Length 90;  
Best Local Similarity 50.0%; Pred. No. 0.15;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
QY 1 GSSFLSP-----AKLQPR 14  
|||  
Db 24 GSSFLSPHQKQAQRKSKKPAKLQPR 51  
|||  
RESULT 13

AAW87991  
ID AAW87991 standard; Protein; 117 AA.  
XX  
XX AAW87991;  
AC  
XX 07-APR-1999 (first entry)  
DT  
XX  
XX Protein designated zsig33.  
DE  
XX  
XX Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;  
KM nutrient absorption regulation; obesity; metabolic disorder.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
XX FH 1..23  
XX Peptide /note="signal peptide"  
FT 24..117  
FT Protein /note="mature protein"  
XX  
XX MO9842840-A1.  
XX  
XX 01-OCT-1998.  
PD  
XX  
XX 23-MAR-1998; 98WO-US05620.  
PF  
XX  
XX 24-MAR-1997; 97US-0822897.  
PR  
XX 24-MAR-1997; 97US-0041102.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
PA  
XX Delsher TA, Sheppard PO;  
PI  
XX  
XX WPI; 1999-070071/06.  
DR N-PSDB; AAX04550.  
XX  
XX Human polypeptide having homology to motilin, zsig33 - useful e.g.  
PT to treat gastrointestinal motility disorders, obesity etc. and to  
PT identify antagonists to treat gastrointestinal hypermotility  
XX  
XX Claim 13; Page 55-56; 69pp; English.  
XX  
XX The present sequence represents a protein designated Zsig33. The nucleic  
CC acids are strongly expressed in stomach tissue. The polypeptide (or  
CC allelic variants/orthologs) can be used to stimulate gastric motility,  
CC measured as increased transit time or gastric emptying of an ingested  
CC substance in mammals. The products are used to treat disorders associated  
CC with gastrointestinal cell contractility, secretion of digestive  
CC enzymes/acids, gastrointestinal motility, recruitment of digestive  
CC enzymes, gastrointestinal inflammation, reflux disease and nutrient  
CC absorption regulation. Zsig33 polypeptides may also be important  
CC neurologically, since the family of gut-brain peptides to which the  
CC homologous protein motilin belongs has been associated with neurological  
CC and CNS functions. They may therefore be used e.g. to regulate satiety  
CC or treat obesity and other metabolic disorders where neurological  
CC feedback modules nutritional absorption. They are useful to identify  
CC zsig33 agonists, antagonists and ligands and to produce antibodies.  
XX  
XX  
SQ Sequence 117 AA;  
Query Match 75.7%; Score 53; DB 20; Length 117;  
Best Local Similarity 50.0%; Pred. No. 0.2;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
QY 1 GSSFLSP-----AKLQPR 14  
|||  
Db 24 GSSFLSPHQRVQQRKSKKPAKLQPR 51  
|||  
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AA87236  
ID AAY87236 standard; Protein; 117 AA.  
XX

AAV87236;  
 11-MAY-2000 (first entry)  
 Human signal peptide containing protein HSPB-13 SEQ ID NO:13.  
 Human; signal peptide-containing protein; HSPB; diagnosis; cancer;  
 inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 antimicrobial; nocrotropic; neuroprotective; cardiovascular; hepatotropic;  
 antiaesthetic; gene therapy; cell proliferation; neurological disorder;  
 reproductive disorder; developmental disorder; arteriosclerosis;  
 cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
 asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 Parkinson's disease; Huntington's disease; ovulatory defect;  
 muscular dystrophy.  
 Homo sapiens.  
 WO200000610-A2.  
 06-JAN-2000.  
 25-JUN-1999; 99WO-US14484.  
 26-JUN-1999; 98US-0090762.  
 31-JUL-1998; 98US-0094983.  
 01-OCT-1998; 98US-0102686.  
 11-DEC-1998; 98US-0112129.  
 (INCYTE PHARM INC.  
 Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
 Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
 Bandman O;  
 WPI; 2000-160673/14.  
 N-PSDB; AAZ98121.  
 New human signal peptide-containing proteins useful in treatment,  
 prevention and diagnosis of e.g. cancer, inflammation and  
 cardiovascular disease  
 Claim 1; Page 168-169; 327pp; English.  
 AAZ98109 to AAZ99242 encode AAV87224 to AAV87357 which represent the  
 human signal peptide-containing proteins HSPB-1 to HSPB-134. HSPBs have  
 anticancer, anti-inflammatory, antimicrobial, nocrotropic, hepatotropic,  
 neuroprotective, cardiovascular and antiaesthetic activities, and can  
 be used in gene therapy. HSPBs can be used to treat or prevent disorders  
 associated with decreased activity or function of HSPB. Antagonists of  
 HSPB are used to treat or prevent disorders associated with increased  
 activity or function of HSPB. Such diseases include cell proliferation  
 (including cancer), inflammation, cardiovascular, neurological,  
 reproductive or developmental disorders, (e.g. arteriosclerosis,  
 cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
 asthma, Crohn's disease, microbial or other infections, congestive or  
 ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
 diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPB  
 nucleic acids can be used for the recombinant production of HSPB, for  
 detecting HSPB in standard hybridisation and amplification assays (for  
 diagnosis and monitoring), in gene therapy, as antisense,  
 triplex-forming or ribozyme therapeutics, for detecting related sequences  
 or genetic variations, and for chromosomal mapping. HSPB are also used to  
 raise specific antibodies (Ab) and to screen for agonists and  
 antagonists (potential therapeutic agents). Ab are used to diagnose, or  
 monitor, HSPB-related diseases (in usual immunoassays), as therapeutic  
 antagonists, in competitive drug screens, and for purification of HSPB  
 from natural sources.  
 Sequence 117 AA;  
 Query Match 75.7%; Score 53; DB 21; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.2;

Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
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 Db 24 GSSFLSPHQRYQGRKSKKPKLQPR 51  
 RESULT 15  
 AAM38890  
 ID AAM38890 standard; Protein, 117 AA.  
 AC AAM38890;  
 XX 22-OCT-2001 (first entry)  
 DT Human polypeptide SEQ ID NO 2035.  
 DE Human; nocrotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 XX peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX Homo sapiens.  
 OS WO200153312-A1.  
 XX 26-JUL-2001.  
 PD 26-DEC-2000; 2000WO-US34263.  
 PF 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Dymnac RT;  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AAI58046.  
 XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX Example 3; SEQ ID NO 2035; 10078pp; English.  
 PS The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 XX the encoded polypeptides (AAM38642-AAI42213) with nocrotropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localized neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX Sequence 117 AA;



Query Match 75.78; Score 53; DB 22; Length 117;  
Best Local Similarity 50.08; Pred. No. 0.2;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
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|||  
Db 24 GSFSLSPENRVRVQQRKESKPPAKLQPR 51  
|||

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Job time : 36 secs

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OM protein - protein search, using SW model

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(without alignments)  
29.423 Million cell updates/sec

Title: MAYES-902-SEQ1  
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Sequence: 1 gsaflspeaklqpr 14

Scoring table: BLOSUM62  
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfllea1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 1          | 53    | 75.7        | 117    | 4  | US-09-046-479-2   |
| 2          | 53    | 75.7        | 117    | 4  | US-08-822-897C-2  |
| 3          | 53    | 75.7        | 117    | 4  | US-09-608-810A-4  |
| 4          | 40    | 57.1        | 11     | 4  | US-09-608-810A-2  |
| 5          | 37    | 52.9        | 417    | 1  | US-07-649-591B-7  |
| 6          | 37    | 52.9        | 417    | 1  | US-08-277-540-7   |
| 7          | 37    | 52.9        | 417    | 1  | US-08-430-787A-7  |
| 8          | 37    | 52.9        | 778    | 4  | US-09-460-145-2   |
| 9          | 37    | 52.9        | 797    | 4  | US-09-460-145-4   |
| 10         | 37    | 52.9        | 913    | 3  | US-08-827-208-3   |
| 11         | 37    | 52.9        | 913    | 4  | US-09-500-358-3   |
| 12         | 37    | 52.9        | 913    | 4  | US-09-498-809-3   |
| 13         | 36    | 51.4        | 57     | 2  | US-08-598-873-36  |
| 14         | 36    | 51.4        | 57     | 2  | US-08-605-430-36  |
| 15         | 35    | 50.0        | 263    | 5  | PCT-US91-08177-13 |
| 16         | 35    | 50.0        | 894    | 4  | US-08-599-455B-2  |
| 17         | 35    | 50.0        | 894    | 4  | US-09-069-781B-2  |
| 18         | 35    | 50.0        | 894    | 4  | US-08-618-957A-12 |
| 19         | 35    | 50.0        | 894    | 4  | US-08-137-132-2   |
| 20         | 35    | 50.0        | 894    | 4  | US-08-864-564A-2  |
| 21         | 35    | 50.0        | 894    | 4  | US-09-094-410-2   |
| 22         | 35    | 50.0        | 895    | 4  | US-08-827-962-19  |
| 23         | 35    | 50.0        | 895    | 4  | US-08-827-962-21  |
| 24         | 35    | 50.0        | 895    | 4  | US-08-640-389A-12 |
| 25         | 35    | 50.0        | 905    | 4  | US-09-369-364A-9  |
| 26         | 35    | 50.0        | 940    | 2  | US-08-938-365-4   |
| 27         | 35    | 50.0        | 941    | 1  | US-08-343-760A-2  |

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|----|----|------|------|---|-------------------|--------------------|
| 28 | 35 | 50.0 | 1162 | 2 | US-08-599-455B-43 | Sequence 43, Appl  |
| 29 | 35 | 50.0 | 1162 | 4 | US-08-827-962-15  | Sequence 15, Appl  |
| 30 | 35 | 50.0 | 1162 | 4 | US-08-827-962-20  | Sequence 20, Appl  |
| 31 | 35 | 50.0 | 1162 | 4 | US-08-803-346-1   | Sequence 1, Appl   |
| 32 | 35 | 50.0 | 1162 | 4 | US-09-069-781B-43 | Sequence 43, Appl  |
| 33 | 35 | 50.0 | 1162 | 4 | US-09-137-132-43  | Sequence 43, Appl  |
| 34 | 35 | 50.0 | 1162 | 4 | US-08-864-564A-43 | Sequence 43, Appl  |
| 35 | 35 | 50.0 | 1162 | 4 | US-09-094-410-43  | Sequence 43, Appl  |
| 36 | 35 | 50.0 | 2353 | 4 | US-08-984-709A-50 | Sequence 50, Appl  |
| 37 | 35 | 50.0 | 2409 | 6 | 5180808-2         | Patent No. 5180808 |
| 38 | 34 | 48.6 | 166  | 2 | US-08-627-610-12  | Sequence 12, Appl  |
| 39 | 34 | 48.6 | 166  | 3 | US-08-384-106A-2  | Sequence 2, Appl   |
| 40 | 34 | 48.6 | 166  | 3 | US-08-384-106A-17 | Sequence 17, Appl  |
| 41 | 34 | 48.6 | 166  | 3 | US-08-384-106A-22 | Sequence 22, Appl  |
| 42 | 34 | 48.6 | 166  | 4 | US-09-240-906-4   | Sequence 4, Appl   |
| 43 | 34 | 48.6 | 166  | 5 | PCT-US96-01643-2  | Sequence 2, Appl   |
| 44 | 34 | 48.6 | 166  | 5 | PCT-US96-05252-4  | Sequence 4, Appl   |
| 45 | 34 | 48.6 | 310  | 4 | US-09-632-947B-8  | Sequence 8, Appl   |

## ALIGNMENTS

RESULT 1  
US-09-046-479-2  
; Sequence 2, Application US/09046479  
; Patent No. 6291653  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Deisher, Theresa A.  
; TITLE OF INVENTION: MOTILIN HOMOLOGS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics, Inc.  
; STREET: 1201 Basslake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/046,479  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A.  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 97-04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-09-046-479-2  
Query Match 75.7%; Score 53; DB 4; Length 117;  
Best Local Similarity 50.0%; Pred. No. 0.015;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 GSSFLSPE-----AKLOPR 14  
 Db 24 GSSFLSPHQRVQQRKSKKPKAKLOPR 51

RESULT 2

US-08-822-897C-2  
 ; Sequence 2, Application US/08822897C  
 ; Patent No. 6380158  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Delsher, Theresa A.  
 ; TITLE OF INVENTION: MOTILIN HOMOLOGS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ZymoGenetics, Inc.  
 ; STREET: 1201 Eastlake Avenue East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/822,897C  
 ; FILING DATE:  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sawlsiak, Deborah A  
 ; REGISTRATION NUMBER: 37,438  
 ; REFERENCE/DOCKET NUMBER: 97-04  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6672  
 ; TELEFAX: 206-442-6678  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 117 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-08-822-897C-2

Query Match 75.7%; Score 53; DB 4; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.015;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 GSSFLSPE-----AKLOPR 14  
 Db 24 GSSFLSPHQRVQQRKSKKPKAKLOPR 51

RESULT 3

US-09-608-810A-4  
 ; Sequence 4, Application US/09608810A  
 ; Patent No. 6420521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Jaepers, Stephen R.  
 ; APPLICANT: Delsher, Theresa A.  
 ; APPLICANT: Bishop, Paul D.  
 ; TITLE OF INVENTION: SGIP PEPTIDES  
 ; FILE REFERENCE: 99-51  
 ; CURRENT APPLICATION NUMBER: US/09/608,810A  
 ; CURRENT FILING DATE: 2000-06-30

;; PRIOR APPLICATION NUMBER: 60/141,592  
 ;; PRIOR FILING DATE: 1999-06-30  
 ;; NUMBER OF SEQ ID NOS: 7  
 ;; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ;; SEQ ID NO 4  
 ;; LENGTH: 117  
 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 ;; FEATURE:  
 ;; NAME/KEY: SIGNAL  
 ;; LOCATION: (1)...(23)  
 ; US-09-608-810A-4

Query Match 75.7%; Score 53; DB 4; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.015;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 GSSFLSPE-----AKLOPR 14  
 Db 24 GSSFLSPHQRVQQRKSKKPKAKLOPR 51

RESULT 4

US-09-608-810A-2  
 ; Sequence 2, Application US/09608810A  
 ; Patent No. 6420521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Jaepers, Stephen R.  
 ; APPLICANT: Delsher, Theresa A.  
 ; APPLICANT: Bishop, Paul D.  
 ; TITLE OF INVENTION: SGIP PEPTIDES  
 ; FILE REFERENCE: 99-51  
 ; CURRENT APPLICATION NUMBER: US/09/608,810A  
 ; CURRENT FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: 60/141,592  
 ; PRIOR FILING DATE: 1999-06-30  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-608-810A-2

Query Match 57.1%; Score 40; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSFLSPE 8  
 Db 1 GSSFLSPE 8

RESULT 5

US-07-649-591B-7  
 ; Sequence 7, Application US/07649591B  
 ; Patent No. 5206161  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dennis Drayna and Daniel Eaton  
 ; TITLE OF INVENTION: No. 5206161e1 Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/649,591B
FILING DATE: 19910201
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-649-591B-7

Query Match      52.9%; Score 37; DB 1; Length 417;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 SSFLSPKALQIP 13
Db      385 SGFLPSRIRKP 396

-RESULT 6
US-08-277-540-7
Sequence 7, Application US/08277540
Patent No. 5474901
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Baton, Dan L.
TITLE OF INVENTION: NO. 5474901el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,540
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
```

```

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-277-540-7

Query Match      52.9%; Score 37; DB 1; Length 417;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 SSFLSPKALQIP 13
Db      385 SGFLPSRIRKP 396

RESULT 7
US-08-430-787A-7
Sequence 7, Application US/08430787A
Patent No. 5593674
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Baton, Dan L.
TITLE OF INVENTION: NO. 5593674el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,787A
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,540
FILING DATE: 19-JUL-1994
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-430-787A-7

Query Match      52.9%; Score 37; DB 1; Length 417;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 SSFLSPKALQIP 13
Db      385 SGFLPSRIRKP 396
```

```
RESULT 8
US-09-460-145-2
; Sequence 2, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; APPLICANT: Song, Chuanzheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,145
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/788,975
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 778 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-460-145-2

Query Match      52.9%; Score 37; DB 4; Length 778;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 SPEAKLOPR 14
Db 668 SPEEQLOPR 676

RESULT 9
US-09-460-145-4
; Sequence 4, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; APPLICANT: Song, Chuanzheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,145
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/788,975
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-460-145-4
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Query Match      52.9%; Score 37; DB 4; Length 797;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 6 SPEAKLOPR 14
Db 687 SPEEQLOPR 695
```

```
RESULT 10
US-08-827-208-3
; Sequence 3, Application US/08827208
; Patent No. 6025178
; GENERAL INFORMATION:
; APPLICANT: Chlou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Striffler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,208
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/014,608
; FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
```

REFERENCE/DOCKET NUMBER: X-10610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 913 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-827-208-3

Query Match 52.9%; Score 37; DB 3; Length 913;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
DB 803 SPEEQLOPR 811

## RESULT 11

US-09-500-358-3  
Sequence 3, Application US/09500358  
Patent No. 6197569

GENERAL INFORMATION:  
APPLICANT: Chlou, Xue-Chiou C.  
APPLICANT: Kramer, Ruth M.  
APPLICANT: Pickard, Richard T.  
APPLICANT: Sharp, John D.  
APPLICANT: Striffler, Beth A.  
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED  
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,358  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,208  
FILING DATE: 28-MAR-1997  
APPLICATION NUMBER: US 60/014,608  
FILING DATE: 29-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/041,264  
FILING DATE: 19-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-10610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 913 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-500-358-3

Query Match 52.9%; Score 37; DB 4; Length 913;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
DB 803 SPEEQLOPR 811

## RESULT 12

US-09-498-809-3

Sequence 3, Application US/09498809  
Patent No. 6242206

GENERAL INFORMATION:  
APPLICANT: Chlou, Xue-Chiou C.  
APPLICANT: Kramer, Ruth M.  
APPLICANT: Pickard, Richard T.  
APPLICANT: Sharp, John D.  
APPLICANT: Striffler, Beth A.  
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED  
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,809  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/827,208  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/041,264  
FILING DATE: 19-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-10610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 913 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-498-809-3

Query Match 52.9%; Score 37; DB 4; Length 913;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
DB 803 SPEEQLOPR 811

## RESULT 13

US-08-598-873-36  
Sequence 36, Application US/08598873  
Patent No. 5928884

GENERAL INFORMATION:

```

: APPLICANT: Croce, Carlo M.
: APPLICANT: Huebner, Kay
: TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
: TITLE OF INVENTION: METHODS BASED THEREON
: NUMBER OF SEQUENCES: 77
: CORRESPONDENCE ADDRESS:
: ADDRESS: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/598,873
: FILING DATE: 09-FEB-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Friebe, Thomas E.
: REGISTRATION NUMBER: 29,258
: REFERENCE/DOCKET NUMBER: 8666-004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 57 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: US-08-598-873-36

Query Match      51.4% Score 36; DB 2; Length 57;
Best Local Similarity 58.3% Pred. No. 8.8;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSFSPKLOPR 13
Db 3 SFISPSCKLOPR 14

RESULT 14
US-08-605-430-36
: Sequence 36, Application US/08605430
: Patent No. 6242212
: GENERAL INFORMATION:
: APPLICANT: Croce, Carlo M.
: APPLICANT: Huebner, Kay
: TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
: TITLE OF INVENTION: METHODS BASED THEREON
: NUMBER OF SEQUENCES: 86
: CORRESPONDENCE ADDRESS:
: ADDRESS: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/605,430
: FILING DATE: 22-FEB-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:

```

```

: NAME: Friebe, Thomas E.
: REGISTRATION NUMBER: 29,258
: REFERENCE/DOCKET NUMBER: 8666-005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 57 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: US-08-605-430-36

Query Match      51.4% Score 36; DB 4; Length 57;
Best Local Similarity 58.3% Pred. No. 8.8;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSFSPKLOPR 13
Db 3 SFISPSCKLOPR 14

RESULT 15
PCT-US91-08177-13
: Sequence 13, Application PC/TUS9108177
: GENERAL INFORMATION:
: APPLICANT: Samal, Siba K
: TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESS: Venable, Baetjer, Howard & Civiletti
: STREET: 1201 New York Avenue N.W., suite 1000
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/08177
: FILING DATE: 19911104
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/608,937
: FILING DATE: 05-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Hieber, David W
: REGISTRATION NUMBER: 30,265
: REFERENCE/DOCKET NUMBER: 20509-96711
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-962-4854
: TELEFAX: 202-962-8300
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 263 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US91-08177-13

Query Match      50.0% Score 35; DB 5; Length 263;
Best Local Similarity 77.8% Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14
Db 224 SPEAKLOPR 232

```



Search completed: January 29, 2003, 13:24:20  
Job time : 15 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 13:21:32 ; Search time 15 Seconds  
(without alignments)  
89.725 Million cell updates/sec

Title: MAYES-902-SEQ1  
Perfect score: 70  
Sequence: 1 gssflspeak1qpr 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 53    | 75.7        | 117    | 1 A59316 | ghrelin precursor  |
| 2          | 53    | 75.7        | 117    | 1 B59316 | ghrelin precursor  |
| 3          | 43    | 61.4        | 248    | 2 PQ0769 | glycoprotein G - b |
| 4          | 43    | 61.4        | 250    | 2 PQ0768 | glycoprotein G - b |
| 5          | 42    | 60.0        | 104    | 2 S73927 | ribosomal protein  |
| 6          | 42    | 60.0        | 105    | 2 B64210 | ribosomal protein  |
| 7          | 41    | 58.6        | 164    | 2 T23249 | hypothetical prote |
| 8          | 41    | 58.6        | 283    | 2 S34851 | hypothetical 31.9K |
| 9          | 40    | 57.1        | 208    | 2 H87334 | conserved hypothet |
| 10         | 40    | 57.1        | 308    | 2 H87306 | glycosyl transfera |
| 11         | 40    | 57.1        | 343    | 2 AB1086 | ATP synthase delta |
| 12         | 40    | 57.1        | 343    | 2 AH1449 | weakly ATP synthas |
| 13         | 40    | 57.1        | 709    | 1 TMBS55 | transcription fact |
| 14         | 39    | 55.7        | 257    | 1 MGNZBR | major surface glyc |
| 15         | 39    | 55.7        | 371    | 2 T49100 | hypothetical prote |
| 16         | 39    | 55.7        | 473    | 2 T46999 | hypothetical prote |
| 17         | 39    | 55.7        | 473    | 2 AC0239 | probable GntR-fam1 |
| 18         | 39    | 55.7        | 558    | 1 A39633 | transcription fact |
| 19         | 39    | 55.7        | 742    | 2 S55098 | probable membrane  |
| 20         | 38.5  | 55.0        | 681    | 2 T01469 | hypothetical prote |
| 21         | 38    | 54.3        | 108    | 2 T04117 | SCC18 protein homo |
| 22         | 38    | 54.3        | 226    | 2 G75342 | hypothetical prote |
| 23         | 38    | 54.3        | 459    | 2 B89927 | hypothetical prote |
| 24         | 38    | 54.3        | 770    | 2 H84463 | hypothetical prote |
| 25         | 36    | 54.3        | 993    | 2 A46415 | basophilic - human |
| 26         | 36    | 54.3        | 1137   | 2 T19414 | hypothetical prote |
| 27         | 36    | 54.3        | 1172   | 2 T00065 | CS6 structural sub |
| 28         | 37    | 52.9        | 154    | 2 I60266 | ctd-p-rha, A-D-glc |
| 29         | 37    | 52.9        | 293    | 2 G98163 |                    |

|    |    |      |      |          |                    |
|----|----|------|------|----------|--------------------|
| 30 | 37 | 52.9 | 293  | 2 AB3124 | glycosyltransferas |
| 31 | 37 | 52.9 | 304  | 2 T46003 | hypothetical prote |
| 32 | 37 | 52.9 | 309  | 2 A38395 | mast cell carboxyp |
| 33 | 37 | 52.9 | 321  | 2 A95182 | hypothetical prote |
| 34 | 37 | 52.9 | 322  | 2 D98049 | thioester-diol     |
| 35 | 37 | 52.9 | 357  | 2 AF0243 | probable exported  |
| 36 | 37 | 52.9 | 391  | 2 T30149 | hypothetical prote |
| 37 | 37 | 52.9 | 417  | 1 A34487 | carboxypeptidase A |
| 38 | 37 | 52.9 | 426  | 2 T00848 | probable serine/th |
| 39 | 37 | 52.9 | 426  | 2 T52285 | serine/threonine-s |
| 40 | 37 | 52.9 | 577  | 2 G83599 | probable gamma-glu |
| 41 | 37 | 52.9 | 603  | 2 A10741 | phosphogluconate d |
| 42 | 37 | 52.9 | 739  | 2 T02996 | N-ethylmaleimide s |
| 43 | 37 | 52.9 | 982  | 2 A53253 | microtubule-associ |
| 44 | 37 | 52.9 | 1152 | 2 A33183 | microtubule-associ |
| 45 | 37 | 52.9 | 1495 | 2 S27001 | alpha-2-macroglobu |

## ALIGNMENTS

RESULT 1  
A59316  
ghrelin precursor - human  
N/Alternate names: preproghrelin  
C/Species: Homo sapiens (man)  
C/Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 21-Jul-2000  
C/Accession: A59316  
R/Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.  
Nature 402, 656-660, 1999  
A/Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.  
A/Reference number: A59316; PMID:20067959; PMID:10604470  
A/Accession: A59316  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-117 <KOJ>  
A/Cross-references: GB:AB029434; NID:G6691571; PIDN:BA09371.1; PID:G6691572  
A/Experimental source: tissue stomach endocrine cells  
A/Note: submitted to GenBank, June 1999  
C/Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (grow-  
C/Keyword: hormone; lipoprotein; stomach  
C/KeyWords: motilin  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-51/Product: ghrelin #status predicted <MAT>  
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CMP>  
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 75.7% ; Score 53; DB 1; Length 117;  
Best Local Similarity 50.0% ; Pred. No. 0.027;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 GSSFLSPR-----AKLQPR 14  
DB 24 GSSFLSPRHQVQORRKKPKLQPR 51

RESULT 2  
B59316  
ghrelin precursor - rat  
N/Alternate names: preproghrelin  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 21-Jul-2000  
C/Accession: B59316  
R/Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.  
Nature 402, 656-660, 1999  
A/Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.  
A/Reference number: A59316; PMID:20067959; PMID:10604470  
A/Accession: B59316  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA; protein  
A/Residues: 1-117 <KOJ>  
A/Cross-references: GB:AB029433; NID:G6691569; PIDN:BA09370.1; PID:G6691570  
A/Experimental source: strain SD; tissue stomach endocrine cells

A>Note: submitted to Genbank, June 1999  
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth)  
C:Superfamily: molitin  
C:Keywords: hormone, lipoprotein, stomach  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-51/Product: ghrelin #status predicted <MAT>  
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 75.7%; Score 53; DB 1; Length 117;  
Best Local Similarity 50.0%; Pred. No. 0.027;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

Oy 1 GSSFLSP-----AKLOPR 14  
Db 24 GSSFLSPHQKQQRKSKKPKAKLOPR 51

RESULT 3  
P00769  
glycoprotein G - bovine respiratory syncytial virus (isolate VC464) (fragment)  
C:Species: bovine respiratory syncytial virus  
C>Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C:Accession: P00769  
R:Mailpeddi, S.K.; Samal, S.K.  
J. Gen. Virol. 74, 2001-2004, 1993  
A:Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial v  
A:Reference number: J02284; MUID:93389461; PMID:8376974  
A:Accession: P00769  
A:Molecule type: mRNA  
A:Residues: 1-248 <MAL>  
A:Experimental source: isolate VC464  
A>Note: the authors translated the codon ACC for residue 85 as His and ATC for residue 2  
C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
C:Keywords: glycoprotein, transmembrane protein  
F:1-29/Domain: intracellular #status predicted <INT>  
F:30-57/Domain: transmembrane #status predicted <TM>  
F:58-248/Domain: extracellular #status predicted <EXT>  
F:76,154,224,242/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 43; DB 2; Length 248;  
Best Local Similarity 88.9%; Pred. No. 4;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 SPEAKLOPR 14  
Db 215 SPEAKLOPR 223

RESULT 4  
P00768  
glycoprotein G - bovine respiratory syncytial virus (isolate FS-1) (fragment)  
C:Species: bovine respiratory syncytial virus  
C>Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C:Accession: P00768  
R:Mailpeddi, S.K.; Samal, S.K.  
J. Gen. Virol. 74, 2001-2004, 1993  
A:Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial v  
A:Reference number: J02284; MUID:93389461; PMID:8376974  
A:Accession: P00768  
A:Molecule type: mRNA  
A:Residues: 1-250 <MAL>  
C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
C:Keywords: glycoprotein, transmembrane protein  
F:1-31/Domain: intracellular #status predicted <INT>  
F:32-59/Domain: transmembrane #status predicted <TM>  
F:60-250/Domain: extracellular #status predicted <EXT>  
F:78,156,226,241,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 43; DB 2; Length 250;  
Best Local Similarity 88.9%; Pred. No. 4.1;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 SPEAKLOPR 14  
Db 217 SPEAKLOPR 225

RESULT 5  
S73927  
ribosomal protein S18 - Mycoplasma pneumoniae (strain ATCC 29342)  
N:Alternate names: hypothetical protein G07\_orf104b  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C>Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
C:Accession: S73927  
R:Himmelreich, R.; Hilbert, H.; Piagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia  
A:Accession number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73927  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-104 <HTM>  
A:Cross-references: EMBL:AE000058; GB:U00089; NID:g1674291; PIDN:AAB96249.1; PID:g16743  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: rps8  
A:Genetic code: SGC3  
C:Superfamily: Escherichia coli ribosomal protein S18  
C:Keywords: protein biosynthesis, ribosome

Query Match 60.0%; Score 42; DB 2; Length 104;  
Best Local Similarity 72.7%; Pred. No. 2.4;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 FLSPYAKINPR 14  
Db 63 FLSPYAKINPR 73

RESULT 6  
B64210  
ribosomal protein S18 - Mycoplasma genitalium  
C:Species: Mycoplasma genitalium  
C>Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 07-Dec-1999  
C:Accession: B64210  
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.  
M.; Fuhmann, J.; Nguyen, D.; Usterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
C.A.; Venter, J.C.  
Science 270, 397-403, 1995  
A:Title: The minimal gene complement of Mycoplasma genitalium.  
A:Reference number: A64200; MUID:96026346; PMID:7569993  
A:Accession: B64210  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-105 <TIGR>  
A:Cross-references: GB:U39688; GB:L43967; NID:g1045753; PID:g1045769; TIGR:MG092  
A:Experimental source: strain G-37  
C:Genetics:  
A:Genetic code: SGC3  
A:Start codon: GTG  
C:Superfamily: Escherichia coli ribosomal protein S18

Query Match 60.0%; Score 42; DB 2; Length 105;  
Best Local Similarity 72.7%; Pred. No. 2.4;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 FLSPYAKINPR 14  
Db 64 FLSPYAKINPR 74

RESULT 7  
T23249  
hypothetical protein K02E2.7 - Caenorhabditis elegans

```

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23249
R:Liroy, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19716
A:Accession: T23249
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-164 <WIL>
A:Cross-references: EMBL:Z81560; PIDN:CAB04544.1; GSPDB:GN00023; CESP:K02E2.7
A:Experimental source: clone K02E2
C:Genetics:
A:Gene: CESP:K02E2.7
A:Map position: 5
A:introns: 35/1; 62/1

Query Match
Best Local Similarity 58.6%; Score 41; DB 2; Length 164;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSFLSPKALQ 13
DB 3 SNFKSPPELQ 14

RESULT 8
S34851
hypothetical 31.9K protein - Streptomyces lavendulae plasmid pSLG33
C:Species: Streptomyces lavendulae
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Sep-1999
C:Accession: S34851
R:Feliseberg, J.; Petricek, M.; Tichy, P.
Nucleic Acids Res. 21, 3582, 1993
A>Title: Nucleotide sequence of the mini-plasmid pSLG33 from Streptomyces lavendulae-gra
A:Reference number: S34850; MUID:93348001; PMID:8346038
A:Accession: S34851
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-283 <FEL>
A:Cross-references: EMBL:X69872
C:Genetics:
A:Genome: plasmid pSLG33
A:Superfamily: Streptomyces lavendulae plasmid pSLG33 hypothetical 31.9K protein

Query Match
Best Local Similarity 58.6%; Score 41; DB 2; Length 283;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GSSFLSPKALQ 13
DB 64 GKDFLSPETKKP 76

RESULT 9
H87334
conserved hypothetical protein CC0691 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87334
R:Nierman, W.C.; Feidbylum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-208 <STO>
A:Cross-references: GB:AE005673; NID:g13421912; PIDN:AAK22676.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0691

```

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Query Match
Best Local Similarity 57.1%; Score 40; DB 2; Length 208;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSSFLSPKALQ 13
DB 108 GATFLNPEARSGP 120

RESULT 10
H87306
glycosyl transferase family protein CC0465 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87306
R:Nierman, W.C.; Feidbylum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87306
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <STO>
A:Cross-references: GB:AE005673; NID:g13421638; PIDN:AAK22452.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0465

Query Match
Best Local Similarity 57.1%; Score 40; DB 2; Length 308;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLSPKALQ 13
DB 105 FLNPDANLQ 114

RESULT 11
AB1086
ATP synthase delta chain homolog lmo0089 [imported] - Listeria monocytogenes (strain EGI
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AB1086
R:Glaser, P.; Frangoul, L.; Buchliesser, C.; Amend, A.; Baguer, F.; Berche, P.; Blocke
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihl, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; M
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A>Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:2157279; PMID:11679669
A:Accession: AB1086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-343 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC98304.1; PID:g16409448; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0089

Query Match
Best Local Similarity 57.1%; Score 40; DB 2; Length 343;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSFLSPKALQ 12
DB 214 SSYLSPKQKX 224

RESULT 12
AH1449

```

weakly ATP synthase delta chain homolog 11n0135 [imported] - *Listeria innocua* (strain C)  
 C:Species: *Listeria innocua*  
 C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
 C:Accession: AH1449  
 R:Glaser, F.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Feigl, H. Science 294, 849-852, 2001  
 A:Authors: Kreft, J.; Kunz, M.; Kuntz, F.; Kurupkat, G.; Madueno, E.; Maitourram, A.; Maok, C.; Schuierer, T.; Simoes, N.; Tixeront, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.  
 A:Reference number: AB1077; MUID:21537279; PMID:11679669  
 A:Accession: AH1449  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-343 <GLA>  
 A:Cross-references: GB:AL592022; PIDN:CA095368.1; PID:G16412554; GSPDB:GN00178  
 A:Experimental source: strain C11p11262  
 C:Genetic8:  
 A:Gene: 11n0135

Query Match 57.1%; Score 40; DB 2; Length 343;  
 Best Local Similarity 72.7%; Pred. No. 20;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SFLSPKALQ 12  
 |||||  
 Db 214 SFLSPKALQ 224

## RESULT 13

TWBY55  
 Transcription factor SM15 [validated] - Yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: protein YD8358.03c; protein YDR146c  
 C:Species: *Saccharomyces cerevisiae*  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000  
 C:Accession: S00342; S57973  
 R:Stillman, D.J.; Bankier, A.T.; Seddon, A.; Groenhouc, E.G.; Nasmyth, K.A. EMBO J. 7, 485-494, 1988  
 A:Title: Characterization of a transcription factor involved in mother cell specific tra  
 A:Reference number: S00342; MUID:88211561; PMID:3284746  
 A:Accession: S00342  
 A:Molecule type: DNA  
 A:Residues: 1-709 <STI>  
 A:Cross-references: EMBL:X06978; NID:G4595; PIDN:CAA30040.1; PID:G4596  
 R:Murphy, L.; Richards, C.; Harris, D.  
 A:Reference number: S57971  
 A:Accession: S57971

A:Molecule type: DNA  
 A:Residues: 1-709 <MUR>  
 A:Cross-references: EMBL:Z50046; NID:G899393; PIDN:CAA90369.1; PID:G899396; GSPDB:GN0000  
 A:Experimental source: strain AB972  
 R:Dutnall, R.N.; Neuhaus, D.; Rhodes, D.  
 A:Reference number: A66200; PDB:1NCS  
 A:Contents: annotation; conformation by (1)H-NMR, residues 532-578  
 R:Neuhaus, D.; Nakaseko, Y.; Schwabe, J.W.R.; Rhodes, D.; Klug, A.  
 A:Reference number: A67819; PDB:1ZPD  
 A:Contents: annotation; conformation by (1)H-NMR, residues 577-608  
 R:Nakaseko, Y.; Neuhaus, D.; Klug, A.; Rhodes, D.  
 J. Mol. Biol. 228, 619-636, 1992  
 A:Title: Adjacent zinc-finger motifs in multiple zinc-finger peptides from SM15 form str  
 A:Reference number: A58624; MUID:93085740; PMID:1453467  
 A:Contents: annotation; conformation by (1)H-NMR  
 R:Neuhaus, D.; Nakaseko, Y.; Schwabe, J.W.R.; Klug, A.  
 J. Mol. Biol. 228, 637-651, 1992  
 A:Title: Solution structures of two zinc-finger domains from SM15 obtained using two-dim

A:Reference number: A58623; MUID:93085741; PMID:1453468  
 A:Contents: annotation; conformation by (1)H-NMR  
 C:Comment: This protein activates the HO gene, which codes for an endonuclease responsib

C:Genetics:  
 A:Gene: SGD:SM15; MIPS:YDR146C  
 A:Cross-references: SGD:S0002553; MIPS:YDR146C  
 A:Map position: 4R

C:Superfamily: transcription factor SM15  
 C:Keywords: DNA binding; metalloprotein; transcription factor; zinc finger  
 F:550-574/Region: zinc finger CCH motif  
 F:580-604/Region: zinc finger CCH motif  
 F:609-632/Region: zinc finger CCH motif  
 F:552,557,570,574/Binding site: zinc (Cys, Cys, His, His) #status experimental  
 F:582,587,600,604/Binding site: zinc (Cys, Cys, His, His) #status experimental  
 F:611,613,626,632/Binding site: zinc (Cys, Cys, His, Cys) #status experimental

Query Match 57.1%; Score 40; DB 1; Length 709;  
 Best Local Similarity 53.8%; Pred. No. 45;  
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 GSFLSPKALQ 13  
 |||||  
 Db 220 GSFLSPKALQ 232

## RESULT 14

MGNZBR  
 major surface glycoprotein G - bovine respiratory syncytial virus (strain 391-2)  
 N:Alternate names: attachment glycoprotein G  
 C:Species: bovine respiratory syncytial virus  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Jul-1999  
 C:Accession: A36408  
 R:Lerch, R.A.; Anderson, K.; Wertz, G.W.  
 J. Virol. 64, 5559-5569, 1990  
 A:Title: Nucleotide sequence analysis and expression from recombinant vectors demonstra  
 Y syncytial virus.

A:Reference number: A36408; MUID:91012801; PMID:2214024  
 A:Accession: A36408  
 A:Molecule type: mRNA  
 A:Residues: 1-257 <LER>  
 A:Cross-references: GB:M58307; NID:G210830; PIDN:AAA42810.1; PID:G210831  
 C:Genetic8:  
 A:Gene: G

C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
 C:Keywords: glycoprotein; transmembrane protein  
 F:45-62/Domain: transmembrane #status predicted <TMN>  
 F:3,85,127,149,233,251/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 257;  
 Best Local Similarity 77.8%; Pred. No. 22;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 SPEAKLQPR 14  
 |||||  
 Db 224 SPEAKLQPR 232

## RESULT 15

T49100  
 hypothetical protein F4F15.320 - *Arabidopsis thaliana*  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
 C:Accession: T49100  
 R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Maché, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.  
 A:Reference number: Z25015  
 A:Accession: T49100

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-371 <ALC>  
 A:Cross-references: EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.320  
 A:Experimental source: cultivar Columbia; BAC clone F4F15

C:Genetics:  
 A:Gene: ATSP:F4F15.320  
 A:Map position: 3  
 A:introns: 34/3; 61/1; 100/1; 151/2; 182/2; 222/2; 252/1; 297/3

Query Match 55.7%; Score 39; DB 2; Length 371;  
Best Local Similarity 50.0%; Pred. No. 34;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GSSFLSPBAKIQPR 14  
DB 233 GPNFVDPGRKLLPR 246

Search completed: January 29, 2003, 13:23:59  
Job time : 16 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 12:58:36 ; Search time 11 Seconds

(without alignments)  
52.788 Million cell updates/sec

Title: MAYES-902-SEQ1

Perfect score: 70

Sequence: 1 gssflspeaklqpr 14

Scoring table: BL0SUM62

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | ID         | Description        |
|------------|-------|-------|-------|--------|------------|--------------------|
| 1          | 53    | 75.7  | 117   | 1      | GHRL_CANFA | Q9be68 canis fam1  |
| 2          | 53    | 75.7  | 117   | 1      | GHRL_HUMAN | Q9ub03 homo sapien |
| 3          | 53    | 75.7  | 117   | 1      | GHRL_MOUSE | Q9eqx0 mus musculi |
| 4          | 53    | 75.7  | 117   | 1      | GHRL_RAT   | Q9qy17 rattus norv |
| 5          | 49    | 70.0  | 118   | 1      | GHRL_PIG   | Q9qky5 sus scrofa  |
| 6          | 43    | 61.4  | 257   | 1      | VGIG_BRSV7 | Q65706 bovine resp |
| 7          | 43    | 61.4  | 257   | 1      | VGIG_BRSVL | Q09495 bovine resp |
| 8          | 43    | 61.4  | 257   | 1      | VGIG_BRSVR | Q84183 bovine resp |
| 9          | 42.5  | 60.7  | 116   | 1      | GHRL_BOVIN | Q9bd16 bos taurus  |
| 10         | 42    | 60.0  | 104   | 1      | RS18_MYCPN | P75541 mycoplasma  |
| 11         | 42    | 60.0  | 105   | 1      | RS18_MYCBE | P47338 mycoplasma  |
| 12         | 40    | 57.1  | 369   | 1      | V181_FOPPV | Q9j552 fowpox vir  |
| 13         | 40    | 57.1  | 369   | 1      | SWIS_YEAST | P08183 saccharomyc |
| 14         | 39.5  | 56.4  | 309   | 1      | ID12_CANAC | Q48965 campotheca  |
| 15         | 39    | 55.7  | 257   | 1      | VGIG_BRSVL | P22261 bovine resp |
| 16         | 39    | 55.7  | 559   | 1      | HNFB_MOUSE | P27889 mus musculi |
| 17         | 39    | 55.7  | 742   | 1      | KM65_YEAST | Q03656 saccharomyc |
| 18         | 38    | 54.3  | 154   | 1      | FEA2_ECOLI | P53599 escherichia |
| 19         | 38    | 54.3  | 961   | 1      | BASO_MOUSE | Q35914 mus musculi |
| 20         | 38    | 54.3  | 994   | 1      | BASO_HUMAN | Q01954 homo sapien |
| 21         | 37    | 52.9  | 154   | 1      | FEA1_ECOLI | P53508 escherichia |
| 22         | 37    | 52.9  | 309   | 1      | PDA2_METMA | P58890 methanosarc |
| 23         | 37    | 52.9  | 309   | 1      | CBPC_RAT   | P21961 rattus norv |
| 24         | 37    | 52.9  | 417   | 1      | CBPC_MOUSE | P15089 mus musculi |
| 25         | 37    | 52.9  | 1152  | 1      | MAP4_HUMAN | P27816 homo sapien |
| 26         | 37    | 52.9  | 1495  | 1      | A2MG_MOUSE | Q61838 mus musculi |
| 27         | 36    | 51.4  | 263   | 1      | LPXA_CAUCR | Q9a715 caulobacter |
| 28         | 36    | 51.4  | 263   | 1      | VGIG_BRSVW | Q10687 bovine resp |
| 29         | 36    | 51.4  | 382   | 1      | ISCC_ARCFU | Q29689 archaeoglob |
| 30         | 36    | 51.4  | 465   | 1      | YHCL_YEAST | P33180 saccharomyc |
| 31         | 36    | 51.4  | 1057  | 1      | SEF1_YEAST | P34228 saccharomyc |
| 32         | 36    | 51.4  | 1072  | 1      | MAP4_BOVIN | P36225 bos taurus  |
| 33         | 36    | 51.4  | 1402  | 1      | IF4G_RABIT | P41110 oryctolagus |

|    |      |      |      |   |            |                     |
|----|------|------|------|---|------------|---------------------|
| 34 | 36   | 51.4 | 1581 | 1 | ARO1_PNECA | Q12659 p pentafunc  |
| 35 | 36   | 51.4 | 1787 | 1 | CHD3_CAEBL | Q22516 caenorhabdi  |
| 36 | 35.5 | 50.7 | 405  | 1 | FLG6_BUCAL | P57422 buchemera ap |
| 37 | 35   | 50.0 | 263  | 1 | VGIG_BRSVL | Q10683 bovine resp  |
| 38 | 35   | 50.0 | 263  | 1 | VGIG_BRSV2 | Q10685 bovine resp  |
| 39 | 35   | 50.0 | 263  | 1 | VGIG_BRSV4 | Q10684 bovine resp  |
| 40 | 35   | 50.0 | 295  | 1 | UL79_HCMVA | P16752 human cytom  |
| 41 | 35   | 50.0 | 355  | 1 | LPXD_AGRT5 | Q8ufl5 agrobacteri  |
| 42 | 35   | 50.0 | 394  | 1 | ARP2_CHICK | P53488 gallus gall  |
| 43 | 35   | 50.0 | 394  | 1 | ARP2_HUMAN | Q5142 homo sapien   |
| 44 | 35   | 50.0 | 395  | 1 | ARP2_DROME | P45888 drosophila   |
| 45 | 35   | 50.0 | 559  | 1 | HNFB_PIG   | Q03365 sus scrofa   |

## ALIGNMENTS

RESULT 1  
GHRL\_CANFA STANDARD; PRT; 117 AA.  
ID GHRL\_CANFA  
AC Q9BEF8; Q9BEF7;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).  
GN GHRL OR MTLRP.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=gastric fundus;  
RA Tomasetto C., Wendling C., Rio M.-C., Poltrae P.;  
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog fundus."  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1/ghrelin (shown here) and 2/dee-ghrelin; are produced by alternative splicing.  
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; A2298295; CAC29155.1; -;  
DR EMBL; A2298296; CAC29156.1; -;  
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;  
KW Alternative splicing.  
FT SIGNAL 1 23 BY SIMILARITY.  
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).  
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).  
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).  
FT VARSPIC 37 37 MISSING (IN ISOFORM 2).  
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;  
Query Match 75.7%; Score 53; DB 1; Length 117;  
Best Local Similarity 50.0%; Pred. No. 0.012;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
QY 1 GSSFLSPE-----AKQPR 14

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Db      24 GSSFLSPHQKQORKESSKPKQPR 51
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RESULT 2
GHR_L_HUMAN STANDARD; PRT; 117 AA.
ID GHR_L_HUMAN
AC Q9UBU3; Q9H3R3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR MTLRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RT stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RA Tomasetto C., Karam S.M., Rio M.-C.;
RT "Identification of a novel gastric protein m46.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajntaj M.P., Ten I.S., Gertner J.M., Leibel R.L.;
RT "Genomic organization of the human Ghrelin gene.";
RL J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE OF 24-33.
RC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RT hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [6]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
RN [7]
RP FUNCTION: Specific ligand for the growth hormone secretagogue
RP receptor type 1 (GHSR) inducing the release of growth hormone from
RP the pituitary. Has an appetite-stimulating effect, induces
RP adiposity and stimulates gastric acid secretion. Involved in
RP growth regulation.
RN [8]
RP SUBCELLULAR LOCATION: Secreted.
RN [9]
RP ALTERNATIVE PRODUCTS: 2 isoforms, 1/ghrelin (shown here) and
RN 2/dea-Gln4-ghrelin; are produced by alternative splicing.
RN [10]
RP PTM: O-n-octanoylation is essential for activity.
RN [11]
RP SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
RN [12]
RP DATABASE: NAME=Acidic Genet. CytoGenet. Oncol. Haematol.;
RN WWW="http://www.infobiogen.fr/services/chromocancer/Genes/Ghrelinid.html".
RN [13]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AB029434; BAA89371.1; -
CC DR EMBL; AB035700; BAB19045.1; -
CC DR EMBL; AJ252278; CAB65733.1; -
CC DR EMBL; AF296558; AAG10300.1; -
CC DR MIM; 605353; -
CC KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
CC Alternative splicing.
CC FT SIGNAL 1 23
CC FT PEPTIDE 24 51 GHRELIN.
CC FT PROPEP 52 117 REMOVED IN MATURE FORM.
CC FT LIPID 26 26 N-OCTANOATE.
CC FT VASPLIC 37 37 MISSING (IN ISOFORM 2).
CC SQ SEQUENCE 117 AA; 12911 MW; 39C0572BDECA2755 CRC64;

Query Match 75.7%; Score 53; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No 0.012; Mismatches 14; Gaps 1;
Matches 14; Conservative 0; Indels 14;

Qy 1 GSSFLSP-----AKQPR 14
Db 24 GSSFLSPHQKQORKESSKPKQPR 51
|||||
RESULT 3
GHR_MOUSE STANDARD; PRT; 117 AA.
ID GHR_MOUSE
AC Q9EQX0; Q9WU21;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR MTLRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
RC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RT hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kojima M.;
RT "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakaishima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217981;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Kynash-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.",  
 RL Nature 409:685-690(2001).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=21203998; PubMed=11306336;  
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;  
 RT "ghrelin: discovery of the natural endogenous ligand for the growth  
 hormone secretagogue receptor.";  
 RL Trends Endocrinol. Metab. 12:118-122(2001).  
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue  
 CC receptor type 1 (GHSR) inducing the release of growth hormone from  
 CC the pituitary. Has an appetite-stimulating effect, induces  
 CC adiposity and stimulates gastric acid secretion. Involved in  
 CC growth regulation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, 1/ghrelin (shown here) and  
 CC 2/dea-Gln14-ghrelin; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract  
 CC with higher levels in the stomach, medium levels in the duodenum,  
 CC jejunum, ileum and colon. Low expression in the testis and brain.  
 CC Not detected in the salivary gland, pancreas, liver and lung.  
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.  
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 CC -----  
 DR EMBL, AJ243503; CAB46500.1; -;  
 DR EMBL, AB035701; BAB19046.1; -;  
 DR EMBL, AB060078; BAB69857.1; -;  
 DR EMBL, AK008658; BAB25814.1; -;  
 DR EMBL, AK008860; BAB25934.1; -;  
 DR MGI, MGI:1930008; Mclrp.  
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;  
 KW Alternative splicing.  
 FT SIGNAL 1 23  
 FT PEPTIDE 51 GHRELIN.  
 FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).  
 FT LIPID 26 N-OCTANOATE (BY SIMILARITY).  
 FT VARSPIC 37 37 MISSING (IN ISOFORM 2).  
 SQ SEQUENCE 117 AA; 13207 MW; EACBA9D2E3CA7203 CRC64;  
 Query Match 75.7%; Score 53; DB 1; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.012;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 QY 1 GSSFLSPS-----AKQPR 14  
 DB 24 GSSFLSPSHQKAOORKESSKPPAKQPR 51  
 RESULT 4  
 GHRH\_RAT STANDARD; PRT; 117 AA.  
 ID GHRH\_RAT  
 AC Q9QYH7; Q9ET69;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone  
 releasing peptide).

GN GHRH.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,  
 RP AND ACYLATION OF SER-26.  
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;  
 RX MEDLINE=20067959; PubMed=10604470;  
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;  
 RT "ghrelin is a growth-hormone-releasing acylated peptide from  
 RT stomach.";  
 RL Nature 402:656-660(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS  
 RP SPECTROMETRY, AND ACYLATION OF SER-26.  
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;  
 RX MEDLINE=20357315; PubMed=10801861;  
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;  
 RT "Purification and characterization of rat dea-Gln14-ghrelin, a second  
 RT endogenous ligand for the growth hormone secretagogue receptor.";  
 RL J. Biol. Chem. 275:21995-22000(2000).  
 RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=21092536; PubMed=1162448;  
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;  
 RT "ghrelin and dea-acyl ghrelin: two major forms of rat ghrelin peptide  
 RT in gastrointestinal tissue.";  
 RL Biochem. Biophys. Res. Commun. 279:909-913(2000).  
 RN [4]  
 RP STRUCTURE-ACTIVITY RELATIONSHIP.  
 RX MEDLINE=2143488; PubMed=11549267;  
 RA Matsumoto M., Hosoda H., Kiritajima Y., Morozumi N., Minamide Y.,  
 RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;  
 RT "Structure-activity relationship of ghrelin: pharmacological study of  
 RT ghrelin peptides.";  
 RL Biochem. Biophys. Res. Commun. 287:142-146(2001).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=21203998; PubMed=11306336;  
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;  
 RT "ghrelin: discovery of the natural endogenous ligand for the growth  
 RT hormone secretagogue receptor.";  
 RL Trends Endocrinol. Metab. 12:118-122(2001).  
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue  
 CC receptor type 1 (GHSR) inducing the release of growth hormone from  
 CC the pituitary. Has an appetite-stimulating effect, induces  
 CC adiposity and stimulates gastric acid secretion. Involved in  
 CC growth regulation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, 1/ghrelin (shown here) and  
 CC 2/dea-Gln14-ghrelin; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Broadly expressed with higher expression in  
 CC the stomach. Very low levels are detected in the hypothalamus,  
 CC heart, lung, pancreas, intestine and adipose tissue.  
 CC -1- PTM: O-n-octanoylation is essential for activity. The replacement  
 CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.  
 CC -1- MASS SPECTROMETRY: MW=3314.9; MW\_ERR=0.7; METHOD=Electrospray;  
 CC RANGE=24-51.  
 CC -1- MASS SPECTROMETRY: MW=3187.1; MW\_ERR=0.6; METHOD=Electrospray;  
 CC RANGE=24-36, 38-51.  
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, AB029433; BAA89370.1; -;

DR EMBL; AB035699; BAB1956.1; -  
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;  
 KM Alternative splicing.  
 FT SIGNAL 1 23  
 FT PEPTIDE 24 51 GHRELIN  
 FT PROPEP 52 117 REMOVED IN MATURE FORM.  
 FT LIPID 26 26 N-OCTANOATE.  
 FT VARSPLIC 37 37 MISSING (IN ISOFORM 2).  
 SQ SEQUENCE 117 AA; 13176 MW; 8857546F5E1A7691 CRC64;  
 Query Match 75.7%; Score 53; DB 1; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.012;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 Oy 1 GSSFLSPPE-----AKLOPR 14  
 |||||  
 Db 24 GSSFLSPPEHQKQKRSKPKAKQPR 51  
 |||||  
 RESULT 5  
 GHRL\_PIG STANDARD; PRT; 118 AA.  
 ID GHRL\_PIG  
 AC 09GKY5; 09GKY4; 09BDG8;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).  
 GN GHRL.  
 OS Sue scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9923;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RA Kojima M.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Stomach;  
 RA Rousselet J.; Lacroix D.; Dubreuil P.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/ghrelin (shown here) and 2/dea-ghn14-ghrelin; are produced by alternative splicing.  
 CC -1- PFM: O-n-octanoylation is essential for activity (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AB035703; BAB19048.1; -  
 DR EMBL; AB035704; BAB19049.1; -  
 DR EMBL; AF308930; AAK19243.1; -  
 DR EMBL; AY028942; AAK30002.1; -  
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;  
 KM Alternative splicing.  
 FT SIGNAL 1 24  
 FT PEPTIDE 25 52 GHRELIN.  
 FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).  
 FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).  
 FT VARSPLIC 38 38 MISSING (IN ISOFORM 2).  
 FT CONFLICT 17 17 L -> P (IN REF. 2; AAK30002).  
 L -> P (IN REF. 2; AAK30002).

FT CONFLICT 72 72 K -> E (IN REF. 2; AAK30002).  
 SQ SEQUENCE 118 AA; 12785 MW; 856D3E1D6DA1A76 CRC64;  
 Query Match 70.0%; Score 49; DB 1; Length 118;  
 Best Local Similarity 46.4%; Pred. No. 0.064;  
 Matches 13; Conservative 1; Mismatches 0; Indels 14; Gaps 1;  
 Oy 1 GSSFLSPPE-----AKLOPR 14  
 |||||  
 Db 25 GSSFLSPPEHQKQKRSKPKAKLKR 52  
 |||||  
 RESULT 6  
 VGLG\_BRSV7 STANDARD; PRT; 257 AA.  
 ID VGLG\_BRSV7  
 AC 065706;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Major surface glycoprotein G (Attachment glycoprotein G).  
 GN G.  
 OS Bovine respiratory syncytial virus (strain 375) (BRV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=82821;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Duncan R.B.; Potgieter L.N.D.;  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
 CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.  
 CC -----  
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 CC -----  
 DR EMBL; L10925; AAA42809.1; -  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoproc\_G.  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37  
 FT TRANSMEM 38 66  
 FT DOMAIN 1 37  
 FT DOMAIN 1 37  
 FT DOMAIN 1 37  
 FT DISULFID 67 257  
 FT DISULFID 173 186  
 FT DISULFID 176 182  
 FT CARBOHYD 85 85  
 FT CARBOHYD 163 163  
 FT CARBOHYD 233 233  
 FT CARBOHYD 248 248  
 FT CARBOHYD 251 251  
 SQ SEQUENCE 257 AA; 28363 MW; F7CE3396305CC015 CRC64;  
 Query Match 61.4%; Score 43; DB 1; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 1.8;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 6 SPEAKIQPR 14  
 |||||  
 Db 224 SPEAKIQPK 232  
 |||||  
 RESULT 7  
 VGLG\_BRSVL

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ID  VGLG_BRSVL  STANDARD;  PRT;  257 AA.
AC  009495;
DT  15-JUL-1998 (Rel. 36, Created)
DT  15-JUL-1998 (Rel. 36, Last sequence update)
DE  15-JUL-1998 (Rel. 36, Last annotation update)
DE  Major surface glycoprotein G (Attachment glycoprotein G).
GN  G.
OS  Bovine respiratory syncytial virus (strain LeJeste) (BRS).
OC  Viruses; ssRNA negative-strand viruses; Mononegavirales;
OX  Paramyxoviridae; Pneumovirinae; Pneumovirus.
RN  NCBI_TaxID=82823;
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9710754; PubMed=9018058;
RA  Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,
RT  Letesson J.J.;
RT  "Antigenic and molecular analyses of the variability of bovine
RT  respiratory syncytial virus G glycoprotein."
RL  J. Gen. Virol. 78:359-366(1997).
CC  -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC  HEMAGGLUTININATING ACTIVITIES.
CC  -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC  -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
CC  HRS VIRUS.
CC  -----
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CC  -----

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DR  EMBL; U35539; AAB50935.1; -.
DR  HSSP; P22261; 1BRV.
DR  InterPro; IPR000925; Glycoprot G.
DR  Pfam; PF00802; Glycoprotein G; 1.
KM  Transmembrane; Glycoprotein.
FT  DOMAIN 1 37
FT  TRANSMEM 38 66
FT  DOMAIN 67 257
FT  DISULFID 173 186
FT  CARBOHYD 176 182
FT  CARBOHYD 85 85
FT  CARBOHYD 163 163
FT  CARBOHYD 233 233
FT  CARBOHYD 251 251
SQ  SEQUENCE 257 AA; 28354 MW; E8DF5710FB21ACDA CRC64;

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Query Match 61.4%; Score 43; DB 1; Length 257;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 6 SPEAKQPR 14
Db 224 SPEAKQPK 232

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```

RESULT 8
VGLG_BRSVR  STANDARD;  PRT;  257 AA.
AC  084183; O12865; O12584;
DT  15-JUL-1998 (Rel. 36, Created)
DT  15-JUL-1998 (Rel. 36, Last sequence update)
DT  15-JUL-1998 (Rel. 36, Last annotation update)
DE  Major surface glycoprotein G (Attachment glycoprotein G).
GN  G.
OS  Bovine respiratory syncytial virus (strain Bb94) (BRS), and
OS  Bovine respiratory syncytial virus (strain 220-69) (BRS).
OC  Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC  Paramyxoviridae; Pneumovirinae; Pneumovirus.

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OX  NCBI_TaxID=11249; 82822;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=RB94;
RX  MEDLINE=9710754; PubMed=9018058;
RA  Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,
RA  Letesson J.J.;
RT  "Antigenic and molecular analyses of the variability of bovine
RT  respiratory syncytial virus G glycoprotein."
RL  J. Gen. Virol. 78:359-366(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=220-69;
RX  MEDLINE=97288324; PubMed=9143302;
RA  Furze J., Roberts S., Wertz G., Taylor G.;
RT  "Antigenically distinct G glycoproteins of BRSV strains share a high
RT  degree of genetic homogeneity."
RL  Virology 231:48-56(1997).
CC  -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC  HEMAGGLUTININATING ACTIVITIES.
CC  -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC  -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
CC  HRS VIRUS.
CC  -----
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DR  EMBL; L27802; AAB47926.1; -.
DR  EMBL; Y08720; CAA69970.1; -.
DR  HSSP; P22261; 1BRV.
DR  InterPro; IPR000925; Glycoprot G.
DR  Pfam; PF00802; Glycoprotein G; 1.
KM  Transmembrane; Glycoprotein.
FT  DOMAIN 1 37
FT  TRANSMEM 38 66
FT  DOMAIN 67 257
FT  DISULFID 173 186
FT  CARBOHYD 176 182
FT  CARBOHYD 85 85
FT  CARBOHYD 163 163
FT  CARBOHYD 233 233
FT  CARBOHYD 251 251
SQ  SEQUENCE 257 AA; 28388 MW; D93E5347FA25FEFF CRC64;

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Query Match 61.4%; Score 43; DB 1; Length 257;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 6 SPEAKQPR 14
Db 224 SPEAKQPK 232

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RESULT 9
GHRL_BOVIN  STANDARD;  PRT;  116 AA.
AC  09BD76; O9GKY6;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE  releasing peptide).
GN  GHRL.
OS  Bos taurus (Bovine).
OS  Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC  Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-99 FROM N.A.
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect. Induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF350329; AAK18612.1; -
DR EMBL; AB035702; BAB19047.1; -
KM Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23
FT PESTIDE 24 50
FT PROPEP 51 116
FT LIPID 26 26
FT CONFLICT 34 34
FT SEQUENCE 116 AA; 12792 MW; F55356DAC5FA59B6 CRC64;
SQ
Query Match 60.7%; Score 42.5; DB 1; Length 116;
Best Local Similarity 84.6%; Pred. No. 0.95;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 GSSFLSPF-AKIQ 12
DQ 24 GSSFLSPF-HOKLO 36
RESULT 10
RS18_MYCPN STANDARD; PRT; 104 AA.
AC P75541;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S18.
GN RPSR OR MPN230 OR MP601.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 29342 / M129;
RA MEDLINE=97105885; PubMed=8948633;
RA Himmelfreith R., Hilbert H., Piagans H., Pirkl E., Li B.-C.,
RA Hermann R.;
RL "Complete sequence analysis of the genome of the bacterium Mycoplasma
RL pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- FUNCTION: This protein has been implicated in aminoacyl-transfer
CC RNA binding. It appears to be situated at the decoding site of
CC messenger RNA (By similarity).
CC -1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; U39689; AAC71310.1; -
DR TIGR; MG092; -
DR InterPro; IPR001648; Ribosomal_S18.
DR Pfam; PFO1084; Ribosomal_S18; 1.
DR PRINTS; PR00974; RIBOSOMALS18.
DR ProDom; PD002239; Ribosomal_S18; 1.
DR TIGRPFAMs; TIGR00165; S18; 1.
DR PROSITE; PS00057; RIBOSOMAL_S18; FALSE NEG.
KM Ribosomal protein; RNA-binding; Complete proteome.
SQ SEQUENCE 104 AA; 12386 MW; 0C424229C79CC1B5 CRC64;

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CC -----
DR EMBL; AEO00058; AAB96249.1; -
DR InterPro; IPR001648; Ribosomal_S18.
DR Pfam; PFO1084; Ribosomal_S18; 1.
DR PRINTS; PR00974; RIBOSOMALS18.
DR ProDom; PD002239; Ribosomal_S18; 1.
DR TIGRPFAMs; TIGR00165; S18; 1.
DR PROSITE; PS00057; RIBOSOMAL_S18; FALSE NEG.
KM Ribosomal protein; RNA-binding; Complete proteome.
SQ SEQUENCE 104 AA; 12386 MW; 0C424229C79CC1B5 CRC64;
Query Match 60.0%; Score 42; DB 1; Length 104;
Best Local Similarity 72.7%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 4 FLSPDAKIQPR 14
DQ 63 FLSPYAKINPR 73
RESULT 11
RS18_MYCPN STANDARD; PRT; 105 AA.
AC P47338;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S18.
GN RPSR OR RPS18 OR MG092.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 33530 / G-37;
RA MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandhu K., Fuhrmann J.L.,
RA Nguyen D.T., Uettermann T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Luster T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RL "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
CC -1- FUNCTION: This protein has been implicated in aminoacyl-transfer
CC RNA binding. It appears to be situated at the decoding site of
CC messenger RNA (By similarity).
CC -1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; U39689; AAC71310.1; -
DR TIGR; MG092; -
DR InterPro; IPR001648; Ribosomal_S18.
DR Pfam; PFO1084; Ribosomal_S18; 1.
DR PRINTS; PR00974; RIBOSOMALS18.
DR ProDom; PD002239; Ribosomal_S18; 1.
DR TIGRPFAMs; TIGR00165; S18; 1.
DR PROSITE; PS00057; RIBOSOMAL_S18; FALSE NEG.
KM Ribosomal protein; RNA-binding; Complete proteome.
SQ SEQUENCE 105 AA; 12463 MW; 0D5F5A1276DF5A26 CRC64;

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Query Match      60.0%; Score 42; DB 1; Length 105;
Best Local Similarity 72.7%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FLSPFLAKOPR 14
    |||||:
    64 FLSPYAKINPR 74

Db

RESULT 12
VIR1_FOWPV      STANDARD; PRT; 369 AA.
ID VIR1_FOWPV
AC 09J552;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE Protein FPV181.
GN FPV181.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Afonso C.L., Tulman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.
CC -----
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CC -----
CC DR EMBL: AF198100; AAF4525.1; -.
CC DR InterPro: IPR004251; DUF230.
CC DR Pfam: PF03003; DUF230; 1.
CC SQ SEQUENCE 369 AA; 42081 MW; 380A71032C18B99 CRC64;

Query Match      57.1%; Score 40; DB 1; Length 369;
Best Local Similarity 88.9%; Pred. No. 9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSFLSPFLAK 10
    |||||
    68 ASFLSPFLAK 76

Db

RESULT 13
SWIS_YEAST      STANDARD; PRT; 709 AA.
ID SWIS_YEAST
AC P08153;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional factor SWIS.
GN SWIS OR YDR146C OR YD8358.03C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88211561; PubMed=3284746;
RA Stillman D.J., Bankier A.T., Seddon A., Groenhout E.G., Naamyn K.A.;
RT "Characterization of a transcription factor involved in mother cell
RT specific transcription of the yeast HO gene.";
RL EMBL J. 7:485-494(1988).

```

```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=3288C / AB972;
RA Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP DNA-BINDING.
RX MEDLINE=88156968; PubMed=2831463;
RA Nagai K., Nakaseko Y., Naamyn K.A., Rhodes D.;
RT "Zinc-finger motifs expressed in E. coli and folded in vitro direct
RT specific binding to DNA.";
RL Nature 332:284-286(1988).
RN [4]
RP PHOSPHORYLATION, MUTAGENESIS, AND INTRACELLULAR LOCALIZATION.
RX MEDLINE=91347374; PubMed=16523372;
RA Moll T., Tebb G., Surana U., Robitsek H., Naamyn K.;
RT "The role of phosphorylation and the CDC28 protein kinase in cell
RT cycle-regulated nuclear import of the S. cerevisiae transcription
RT factor SWIS.";
RL Cell 66:743-758(1991).
RN [5]
RP STRUCTURE BY NMR OF 540-608
RX MEDLINE=93085741; PubMed=1453468;
RA Neuhaus D., Nakaseko Y., Schwabe J.W.R., Klug A.;
RT "Solution structures of two zinc-finger domains from SWIS obtained
RT using two-dimensional 1H nuclear magnetic resonance spectroscopy. A
RT zinc-finger structure with a third strand of beta-sheet.";
RL J. Mol. Biol. 228:637-651(1992).
CC -1- FUNCTION: DETERMINES THE MOTHER-CELL-SPECIFIC TRANSCRIPTION OF THE
CC HO ENDONUCLEASE GENE THAT IS RESPONSIBLE FOR THE INITIATION OF
CC MATING-TYPE SWITCHING IN YEAST. RECOGNIZES A SPECIFIC SEQUENCE IN
CC THE PROMOTOR OF THE HO GENE. ACTIVATES EGT2 TRANSCRIPTION IN A
CC CONCENTRATION-DEPENDENT MANNER. SYNTHESIZED DURING G2 AND EARLY
CC MITOSIS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR IN G1, BUT CYTOPLASMIC IN S, G2, AND
CC M CELL CYCLE PHASES.
CC -1- PTM: CELL CYCLE-DEPENDENT PHOSPHORYLATION OF THREE SERINE RESIDUES
CC PREVENTS SWIS FROM ENTERING THE NUCLEUS, AND IT ACCUMULATES IN THE
CC CYTOPLASM. AS A CONSEQUENCE OF CDC28 KINASE INACTIVATION AT THE
CC END OF ANAPHASE, THE THREE SERINE RESIDUES ARE DEPHOSPHORYLATED
CC AND SWIS ENTERS THE NUCLEUS TO ACTIVATE TRANSCRIPTION. IT IS THEN
CC RAPIDLY DEGRADED. THREONINE PHOSPHORYLATION ALSO SEEMS TO OCCUR.
CC -1- SIMILARITY: STRONG, TO YEAST METALLOTHIONEIN EXPRESSION ACTIVATOR
CC ACE2.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: X06978; CAA30040.1; -.
CC DR EMBL: Z50046; CAA30369.1; -.
CC DR PIR: S00342; TWBY55.
CC DR PDB: 1NCS; 10-TUL-96.
CC DR PDB: 1ZFD; 14-OCT-96.
CC DR TRANSPAC: T00776; -.
CC DR SGD: S0002553; SWIS.
CC DR InterPro: IPR000637; AT hook.
CC DR InterPro: IPR000822; ZnF_C2H2.
CC DR Pfam: PF00096; ZF-C2H2; 3.
CC DR PRINTS: PR02178; AT_hook; 1.
CC DR SMART: SM00384; AT_hook; 1.
CC DR SMART: SM00355; ZnF_C2H2; 2.
CC DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 2.
CC DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 2.
CC DR Transcription regulation; Activator; Zinc-finger; DNA-binding;
CC Repeat; Metal-binding; Nuclear protein; Phosphorylation;
CC 3D-structure.

```



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FT DOMAIN 550 632 ZINC FINGERS.
FT ZN_FING 550 574 C2H2-TYPE.
FT ZN_FING 580 604 C2H2-TYPE.
FT ZN_FING 609 632 C2H2-TYPE.
FT SITE 635 659 NUCLEAR TARGETING SIGNAL (POTENTIAL).
FT MOD_RES 522 522 PHOSPHORYLATION (BY CDC28).
FT MOD_RES 646 646 PHOSPHORYLATION (BY CDC28).
FT MOD_RES 664 664 PHOSPHORYLATION (BY CDC28).
FT MUTAGEN 522 522 S->A: CONSTITUTIVE NUCLEAR ENTRY; WHEN ASSOCIATED WITH A-646 AND A-664.
FT MUTAGEN 646 646 S->A: CONSTITUTIVE NUCLEAR ENTRY; WHEN ASSOCIATED WITH A-522 AND A-664.
FT MUTAGEN 664 664 S->A: CONSTITUTIVE NUCLEAR ENTRY; WHEN ASSOCIATED WITH A-522 AND A-646.
FT SEQUENCE 709 AA; 79775 MW; BEF5ED5BFB6E30F6 CRC64;

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```

Query Match 57.1%; Score 40; DB 1; Length 709;
Best Local Similarity 53.8%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Oy 1 GSFSPKALQPR 13
Db 220 GPFSPKALQPR 232

```

## RESULT 14

```

ID ID2 CAMAC STANDARD; PRT: 309 AA.
AC 048965;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Isolepenthyl-diphosphate delta-isomerase II (EC 5.3.3.2) (IPP isomerase II) (Isolepenthyl pyrophosphate isomerase II).
GN IIP2.
OS Camptotheca acuminata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Cornales; Myrsineae; Camptotheca.
OX NCBI_TaxID=16922;
RN [1]
RP SEQUENCE FROM N.A.
RA Jung K.-H., Christensen D.J., Scott A.I.;
RT "Isolation and characterization of two genes from Camptotheca acuminata that encode isopentenyl diphosphate isomerase.";
RL Submitted (0CT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE 1,3-ALLYLIC REARRANGEMENT OF THE HOMOMALLYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS ALLYLIC ISOMER, DIMETHYLLALLYL DIPHOSPHATE (DMAPP) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: isopentenyl diphosphate = dimethylallyl diphosphate.
CC -1- PATHWAY: Chlorophyll biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE 1 FAMILY.
CC -----
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CC -----
DR EMBL; AF031080; AAB94133.1; -.
DR InterPro; IPR002667; IPP_isomerase.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX_1.
DR ProDom; PD004109; IPP_isomerase; 1.
KW Isomerase; Isoprene biosynthesis; Photosynthesis;
KW Chlorophyll biosynthesis.
FT ACT_SITE 163 163 BY SIMILARITY.
FT ACT_SITE 225 225 BY SIMILARITY.
SQ SEQUENCE 309 AA; 35205 MW; BAF51CF8D2ED04 CRC64;

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Query Match 56.4%; Score 39.5; DB 1; Length 309;
Best Local Similarity 71.4%; Pred. No. 9.2;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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Oy 2 SSFL-SPEAKLQPR 14
Db 16 SSFLASPKLQPR 29

```

## RESULT 15

```

ID ID2 BRVVC STANDARD; PRT: 257 AA.
AC P22261;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Bovine respiratory syncytial virus (strain Copenhagen) (BRV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11248;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91012801; PubMed=2214024;
RA Lerch R.A., Anderson K., Wertz G.W.;
RT "Nucleotide sequence analysis and expression from recombinant vectors demonstrate that the attachment protein G of bovine respiratory syncytial virus is distinct from that of human respiratory syncytial virus."
RL J. Virol. 64:5559-5569(1990).
RN [2]
RP STRUCTURE BY NMR OF 156-189.
RC STRAIN=391-2.
RX MEDLINE=97098087; PubMed=8942628;
RA Doreleijers J.F., Langedijk J.P.M., Haard K., Boelens R., Rullmann J.A., Schaper W.M., Van Oirschot J.T., Kaptein R.;
RT "Solution structure of the immunodominant region of protein G of bovine respiratory syncytial virus."
RL Biochemistry 35:14684-14688(1996).
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.
CC -----
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CC -----
DR EMBL; M58307; AAA42810.1; -.
DR PIR; A36408; MENZER.
DR PDB; 1BRV; 05-JUN-97.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein G; 1.
KW Transmembrane; Glycoprotein; 3D-structure.
FT DOMAIN 1 37 CYTOPLASMIC.
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 257 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186
FT DISULFID 176 182
FT CARBOHYD 85 85
FT CARBOHYD 127 127
FT CARBOHYD 233 233
FT CARBOHYD 251 251
SQ SEQUENCE 257 AA; 28569 MW; 0B86D541FBA0657D CRC64;

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Query Match . 55.7%; Score 39; DB 1; Length 257;  
 Best Local Similarity 77.8%; Pred. No. 9.4;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 6 SPEAKLOPR 14  
 Db 224 SPETKLOPK 232

Search completed: January 29, 2003, 13:23:01  
 Job time : 13 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 13:19:02 ; Search time 29 Seconds  
(without alignments)  
99.471 Million cell updates/sec

Title: MAYES-902-SEQ1  
Perfect score: 70  
Sequence: 1 gssflspeaklqpr 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 53    | 75.7        | 117    | 4     | Q8TAT9      |
| 2          | 43    | 61.4        | 251    | 12    | P89309      |
| 3          | 43    | 61.4        | 251    | 12    | P90378      |
| 4          | 43    | 61.4        | 251    | 12    | P89310      |
| 5          | 43    | 61.4        | 257    | 12    | Q9YNF9      |
| 6          | 43    | 61.4        | 257    | 12    | Q9YNF8      |
| 7          | 43    | 61.4        | 257    | 12    | Q9YNF7      |
| 8          | 43    | 61.4        | 257    | 12    | Q9YNF6      |
| 9          | 43    | 61.4        | 257    | 12    | Q9YNF5      |
| 10         | 43    | 61.4        | 257    | 12    | Q9YNF4      |
| 11         | 43    | 61.4        | 257    | 12    | Q9YNF3      |
| 12         | 41    | 58.6        | 164    | 5     | Q9XUV5      |
| 13         | 41    | 58.6        | 164    | 11    | Q9DBT6      |
| 14         | 41    | 58.6        | 815    | 2     | Q47732      |
| 15         | 40    | 57.1        | 96     | 16    | Q98F99      |
| 16         | 40    | 57.1        | 208    | 16    | Q9AAB3      |

|    |      |      |      |    |        |
|----|------|------|------|----|--------|
| 17 | 40   | 57.1 | 252  | 2  | P70866 |
| 18 | 40   | 57.1 | 256  | 2  | Q9S0A7 |
| 19 | 40   | 57.1 | 308  | 16 | Q9AAX7 |
| 20 | 40   | 57.1 | 343  | 16 | Q92FHI |
| 21 | 40   | 57.1 | 343  | 16 | Q8YAM9 |
| 22 | 40   | 57.1 | 470  | 3  | Q8X0Z2 |
| 23 | 40   | 57.1 | 680  | 11 | Q921G6 |
| 24 | 40   | 57.1 | 1078 | 5  | Q9NDY3 |
| 25 | 39   | 55.7 | 188  | 16 | Q92KNO |
| 26 | 39   | 55.7 | 251  | 12 | P89311 |
| 27 | 39   | 55.7 | 371  | 10 | Q9SUT4 |
| 28 | 39   | 55.7 | 435  | 11 | Q8RI62 |
| 29 | 39   | 55.7 | 469  | 11 | Q9CS26 |
| 30 | 39   | 55.7 | 473  | 16 | Q9ZC65 |
| 31 | 39   | 55.7 | 532  | 11 | Q9RIW2 |
| 32 | 39   | 55.7 | 532  | 11 | Q9WTL6 |
| 33 | 39   | 55.7 | 558  | 11 | Q9WTL5 |
| 34 | 39   | 55.7 | 558  | 11 | Q9RIW1 |
| 35 | 39   | 55.7 | 991  | 5  | Q9VIF5 |
| 36 | 39   | 55.7 | 1335 | 11 | Q8VIL7 |
| 37 | 39   | 55.7 | 1336 | 11 | Q9ES55 |
| 38 | 38.5 | 55.0 | 681  | 10 | Q81436 |
| 39 | 38   | 54.3 | 103  | 11 | Q8VD22 |
| 40 | 38   | 54.3 | 108  | 10 | Q40737 |
| 41 | 38   | 54.3 | 187  | 17 | Q970U3 |
| 42 | 38   | 54.3 | 226  | 16 | Q9RT86 |
| 43 | 38   | 54.3 | 322  | 5  | Q45024 |
| 44 | 38   | 54.3 | 406  | 3  | Q9PBD1 |
| 45 | 38   | 54.3 | 459  | 16 | Q99U08 |

## ALIGNMENTS

RESULT 1  
ID Q8TAT9 PRELIMINARY; PRT; 117 AA.  
AC Q8TAT9;  
DT 01-JUN-2002 (T-REMBLrel. 21, Created)  
DT 01-JUN-2002 (T-REMBLrel. 21, Last sequence update)  
DE Ghrelin.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=BLOOD;  
RA Strausberg R.;  
DR EMBL; BC025791; AAH25791.1; -  
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;  
  
Query Match 75.7%; Score 53; DB 4; Length 117;  
Best Local Similarity 50.0%; Pred. No. 0.031;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
  
QY 1 GSSFLSPE-----AKLQPR 14  
DB 24 GSSFLSPEHORVOQRKSKPKPAKLQPR 51  
  
RESULT 2  
ID P89309 PRELIMINARY; PRT; 251 AA.  
AC P89309;  
DT 01-MAY-1997 (T-REMBLrel. 03, Created)  
DT 01-MAY-1997 (T-REMBLrel. 03, Last sequence update)  
DT 01-MAR-2002 (T-REMBLrel. 20, Last annotation update)  
DE Attachment glycoprotein (Fragment).  
GN G.  
OS Bovine respiratory syncytial virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 NCBI\_TaxId=11246;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=NMK7;  
 MEDLINE=91170754; PubMed=9018058;  
 RA Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,  
 Leeseon J.J.;  
 RT "Antigenic and molecular analyses of the variability of bovine  
 respiratory syncytial virus G glycoprotein.";  
 RL J. Gen. Virol. 78:359-366(1997).  
 DR EMBL; U24713; AAC56940.1; -.  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 251 AA; 27467 MW; CED605DD49103DC3 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 251;  
 Best Local Similarity 88.9%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 218 SPEAKLOPK 226

RESULT 3  
 P90378 PRELIMINARY; PRT; 251 AA.  
 AC P90378;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Attachment glycoprotein (Fragment).  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 NCBI\_TaxId=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MVRS53;  
 RX MEDLINE=91170754; PubMed=9018058;  
 RA Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,  
 Leeseon J.J.;  
 RT "Antigenic and molecular analyses of the variability of bovine  
 respiratory syncytial virus G glycoprotein.";  
 RL J. Gen. Virol. 78:359-366(1997).  
 DR EMBL; U24714; AAC56941.1; -.  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 251 AA; 27680 MW; BE11B3B1B0FB8435 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 251;  
 Best Local Similarity 88.9%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 218 SPEAKLOPK 226

RESULT 4  
 P89310 PRELIMINARY; PRT; 251 AA.  
 ID P89310

AC P89310;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Attachment glycoprotein (Fragment).  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 NCBI\_TaxId=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DORSSET;  
 RX MEDLINE=91170754; PubMed=9018058;  
 RA Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,  
 Leeseon J.J.;  
 RT "Antigenic and molecular analyses of the variability of bovine  
 respiratory syncytial virus G glycoprotein.";  
 RL J. Gen. Virol. 78:359-366(1997).  
 DR EMBL; U24715; AAC56942.1; -.  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 251 AA; 27643 MW; 7786571D0EFF9D51 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 251;  
 Best Local Similarity 88.9%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 218 SPEAKLOPK 226

RESULT 5  
 Q9YNF9 PRELIMINARY; PRT; 257 AA.  
 AC Q9YNF9;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 NCBI\_TaxId=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=8307027;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Utenthal A., Arcander P., Tjornehoj K., Vluuf B.,  
 Ronved C., Ronsholt L., Alexandersen S., Blixenkrone-Moller M.,  
 RT "Serological and genetic characterization of bovine respiratory  
 syncytial virus (BRV) indicates that Danish isolates belong to the  
 intermediate subgroup: no evidence of a selective effect on the  
 RT adaptation and passages in cell culture or calves.";  
 RL Vet. Microbiol. 62:265-279(1998).  
 DR EMBL; U92098; AAD00710.1; -.  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
 SQ SEQUENCE 257 AA; 28288 MW; C3106210BAC2817 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKQPR 14  
 |||||  
 Db 224 SPEAKQPR 232

## RESULT 6

Q9YNF8 PRELIMINARY; PRT; 257 AA.  
 ID Q9YNF8;  
 AC Q9YNF7;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=87L0195;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenchal A., Arcander P., Tjornehoj K., Vinuf B.,  
 RA Rontved C., Ronsholt L., Alexandersen S., Blixenkron-Moller M.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup: no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptin and passages in cell culture or calves.";  
 RL Vet. Microbiol. 62:265-279(1998).  
 DR EMBL; U92100; AAD00712.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne\_attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28324 MW; 94EB8BC358739B8 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKQPR 14  
 |||||  
 Db 224 SPEAKQPR 232

RESULT 7  
 Q9YNF7 PRELIMINARY; PRT; 257 AA.  
 ID Q9YNF7;  
 AC Q9YNF7;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9304899;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenchal A., Arcander P., Tjornehoj K., Vinuf B.,  
 RA Rontved C., Ronsholt L., Alexandersen S., Blixenkron-Moller M.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup: no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptin and passages in cell culture or calves.";  
 RL Vet. Microbiol. 62:265-279(1998).

DR EMBL; U92101; AAD00713.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne\_attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28380 MW; 6BD146B3B02E5ACB CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKQPR 14  
 |||||  
 Db 224 SPEAKQPR 232

## RESULT 8

Q9YNF6 PRELIMINARY; PRT; 257 AA.  
 ID Q9YNF6;  
 AC Q9YNF6;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9314893;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenchal A., Arcander P., Tjornehoj K., Vinuf B.,  
 RA Rontved C., Ronsholt L., Alexandersen S., Blixenkron-Moller M.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup: no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptin and passages in cell culture or calves.";  
 RL Vet. Microbiol. 62:265-279(1998).  
 DR EMBL; U92102; AAD00714.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne\_attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28421 MW; 940C1EB22895BD02 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKQPR 14  
 |||||  
 Db 224 SPEAKQPR 232

## RESULT 9

Q9YNF5 PRELIMINARY; PRT; 257 AA.  
 ID Q9YNF5;  
 AC Q9YNF5;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=9402020;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenhal A., Arcander P., Tjornehoj K., Viuff B.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup; no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptation and passages in cell culture or calves."  
 RL Vet. Microbiol. 62:265-279(1998).  
 DR EMBL; U92103; AAD00715.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 2838 MW; C1A2D5BECT6592E CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 SPEAKLOPR 14  
 Db 224 SPEAKLOPK 232

RESULT 10  
 O9YNF4 PRELIMINARY; PRT; 257 AA.  
 AC O9YNF4;  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9402022;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenhal A., Arcander P., Tjornehoj K., Viuff B.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup; no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptation and passages in cell culture or calves."  
 RL Vet. Microbiol. 62:265-279(1998).  
 DR EMBL; U92104; AAD00716.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28379 MW; C1A2D36ECL657LE CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 SPEAKLOPR 14  
 Db 224 SPEAKLOPK 232

RESULT 11  
 O9YS25 PRELIMINARY; PRT; 257 AA.

AC O9YS25;  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus, and  
 OS Bovine respiratory syncytial virus (strain A51908) (BRS).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246; 11247;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine respiratory syncytial virus; STRAIN=ATUES1908;  
 RX MEDLINE=99102581; PubMed=9847328;  
 RA Buchholz U.J., Finke S., Conzelmann K.K.;  
 RT "Generation of bovine respiratory syncytial virus (BRSV) from cDNA:  
 RT BRSV NS2 is not essential for virus replication in tissue culture, and  
 RT the human RSV leader region acts as a functional BRSV genome  
 RT promoter."  
 RL J. Virol. 73:251-259(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine respiratory syncytial virus; STRAIN=ATUES1908;  
 RA Buchholz U.J., Finke S., Conzelmann K.-K.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine respiratory syncytial virus (strain A51908) (BRS);  
 RX MEDLINE=21580793; PubMed=11724268;  
 RA Yunus A.S., Khatlat S.K., Collins P.L., Samal S.K.;  
 RT "Rescue of bovine respiratory syncytial virus from cloned cDNA: entire  
 RT genome sequence of BRSV strain A51908."  
 RL Virus Genes 23:157-164(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine respiratory syncytial virus (strain A51908) (BRS);  
 RA Yunus A.S., Khatlat S.K., Collins P.L., Samal S.K.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF992942; AAC96307.1; -.  
 DR EMBL; AF298543; AAL49398.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28479 MW; 3AE078372A0FEBIF CRC64;

Query Match

61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 SPEAKLOPR 14  
 Db 224 SPEAKLOPK 232

RESULT 12  
 O9XUV5 PRELIMINARY; PRT; 164 AA.  
 AC O9XUV5;  
 DT 01-NOV-1999 (TRENBLrel. 12, Created)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE k0252.7 protein.  
 GN k0252.7.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lloyd C.R.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode *C.elegans*: A platform for  
 investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL; Z81560; CAB04544.1; -.  
 SO SEQUENCE 164 AA; 19025 MW; 4208E365751CBCT70 CRC64;

Query Match 58.6%; Score 41; DB 5; Length 164;  
 Best Local Similarity 66.7%; Pred. No. 8.4;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 3 SNFSPSPKLOP 14

RESULT 13

09DBT6 PRELIMINARY; PRT; 624 AA.

ID 09DBT6;  
 DT 01-JUN-2001 (TEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)  
 DE 1200014E20R1K protein.  
 GN TNS OR 1200014E20R1K.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=LUNG;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Maehio T.,  
 RA Sakai K., Orido T., Furuno M., Aono H., Baldarelli R., Barch G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK004758; BAB23539.1; -.  
 DR HSSP; P16277; 1BLK.  
 DR MGD; MGI:104552; Tns.  
 DR InterPro; IPR000050; PID domain.  
 DR InterPro; IPR000980; SH2-  
 DR Pfam; PF00017; SH2; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00462; PTK; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR PROSITE; PSS0001; SH2; 1.  
 SO SEQUENCE 624 AA; 65369 MW; 296FC3741EFC57E CRC64;

Query Match 58.6%; Score 41; DB 11; Length 624;  
 Best Local Similarity 61.5%; Pred. No. 36;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GSSFLSPKLOP 13  
 Db 31 GSSYNSPDYSLQ 43

RESULT 14

047732 PRELIMINARY; PRT; 815 AA.

ID 047732;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)  
 DE ORF16.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Enterococcaceae; Enterococcus.  
 ON NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DS16; TRANSPOSON=TN916;  
 RX MEDLINE=95207419; PubMed=7899523;  
 RA Piamagan S.E., Zitzow L.A., Su Y.A., Clewell D.B.;  
 RT "Nucleotide sequence of the 18-kb conjugative transposon Tn916 from  
 Enterococcus faecalis."  
 RL Plasmid 32:350-354(1994).  
 DR EMBL; U09422; AAB60017.1; -.  
 SO SEQUENCE 815 AA; 93317 MW; 594C6A5F4FC59867 CRC64;

Query Match 58.6%; Score 41; DB 2; Length 815;  
 Best Local Similarity 80.0%; Pred. No. 48;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 32 SFLSPKLOQ 41

RESULT 15

098F99 PRELIMINARY; PRT; 96 AA.

ID 098F99;  
 DT 01-OCT-2001 (TEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TEMBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein msr3871.  
 GN MSR3871.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 ON NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,  
 RA Wochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti."  
 RL DNA Res. 7:331-336(2000).  
 DR EMBL; AP003002; BAB50668.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 96 AA; 10602 MW; 586EDA57D76BA225 CRC64;

Query Match 57.1%; Score 40; DB 16; Length 96;  
 Best Local Similarity 66.7%; Pred. No. 7.2;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSSFLSPKLOQ 12

Db 14 GSSMLQPKAELO 25

Search completed: January 29, 2003, 13:23:37  
Job time : 31 secs

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